

Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		
			100					105					110				
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc		384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly		
		115					120					125					
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac		432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		
	130					135					140						
aac	tac	atc	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag				474
Asn	Tyr	Ile	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln				
145					150					155							

<210> 535

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1DX, Y66W, N146I, and M153T mutations

<400> 535

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu		
1				5					10					15			

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		
			20					25					30				

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile		
		35					40					45					

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
	50					55					60						

Phe	Gly	Trp	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys		
65					70					75					80		

Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		
			85						90					95			

Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		
			100					105					110				

Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly		
		115					120					125					

Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		
	130					135					140						

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
 145 150 155

<210> 536
 <211> 471
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1DX, Y66W, N146I, and M153T mutations,
 and posit. 1 Met removed

<220>
 <221> CDS
 <222> (1)..(471)

<400> 536
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30
 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60
 ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140
 tac atc agc cac aac gtc tat atc acc gcc gac aag cag 471
 Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
 145 150 155

<210> 537
 <211> 157
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1DX, Y66W, N146I, and M153T mutations,
 and posit. 1 Met removed

<400> 537

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
 145 150 155

<210> 538
 <211> 474
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1DX, with S65A mutation

<220>
 <221> CDS
 <222> (1)..(474)

 <400> 538
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

 ttc gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

 atc gac ttc aag gag gac ggc aac atc ctg ggc cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

 aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag 474
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

 <210> 539
 <211> 158
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; CFP F1DX, with S65A mutation

 <400> 539
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

<210> 540
 <211> 471
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1DX, w. S65A mutation, and posit. 1
 Met removed

<220>
 <221> CDS
 <222> (1)..(471)

<400> 540
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys

35

40

45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag	471
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
145 150 155	

<210> 541
 <211> 157
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1DX, w. S65A mutation, and posit. 1
 Met removed

<400> 541

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 542
<211> 474
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; CFP F1DX, S65A, Y66W, and S72A mutations

<220>
<221> CDS
<222> (1)..(474)

<400> 542
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60
ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336

Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		
			100					105					110				
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc		384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly		
		115					120					125					
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac		432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		
	130					135					140						
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag				474
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln				
145					150					155							

<210> 543

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1DX, S65A, Y66W, and S72A mutations

<400> 543

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu		
1				5					10					15			

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		
			20					25					30				

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile		
		35					40					45					

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
	50					55					60						

Phe	Ala	Trp	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys		
65					70					75					80		

Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		
			85						90					95			

Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		
			100					105					110				

Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly		
		115					120					125					

Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		
	130					135					140						

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

<210> 544

<211> 471

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1DX, S65A, Y66W, and S72A mutations, and
 posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(471)

<400> 544

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag 471
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

<210> 545
 <211> 157
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1DX, S65A, Y66W, and S72A mutations, and
 posit. 1 Met removed

<400> 545

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

<210> 546
 <211> 474
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; BFP F1DX, with Y66H mutation

<220>
 <221> CDS
 <222> (1)..(474)

 <400> 546
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

 ttc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

 aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag 474
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

<210> 547
 <211> 158
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; BFP F1DX, with Y66H mutation

<400> 547

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

20	25	30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
35	40	45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
50	55	60	
Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys			
65	70	75	80
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
85	90	95	
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
100	105	110	
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
115	120	125	
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130	135	140	
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln			
145	150	155	
<210> 548			
<211> 471			
<212> DNA			
<213> Artificial			
<220>			
<223> modif. frag.; BFP F1DX, w. Y66H mutation, and posit. 1 Met removed			
<220>			
<221> CDS			
<222> (1)..(471)			
<400> 548			
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc			48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val			
1 5 10 15			
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag			96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu			
20 25 30			
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc			144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys			
35 40 45			

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag 471
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

<210> 549
 <211> 157
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; BFP F1DX, w. Y66H mutation, and posit. 1 Met
 removed

<400> 549

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 550
<211> 474
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; BFP F1DX, w. F64L, Y66H mutations

<220>
<221> CDS
<222> (1)..(474)

<400> 550
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60
ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

100	105	110	
gtg aag ttc gag ggc gac acc	ctg gtg aac cgc atc	gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr	Leu Val Asn Arg Ile	Glu Leu Lys Gly	
115	120	125	
atc gac ttc aag gag gac ggc	aac atc ctg ggg cac aag	ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly	Asn Ile Leu Gly His Lys	Leu Glu Tyr	
130	135	140	
aac tac aac agc cac aac gtc	tat atc atg gcc gac aag	cag	474
Asn Tyr Asn Ser His Asn Val	Tyr Ile Met Ala Asp Lys	Gln	
145	150	155	

<210> 551

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F1DX, w. F64L, Y66H mutations

<400> 551

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 552
 <211> 471
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; BFP F1DX, w. F64L, Y66H mutations, and
 posit. 1 Met removed

<220>
 <221> CDS
 <222> (1)..(471)

<400> 552

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
50 55 60	
ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag	471
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	
145 150 155	

<210> 553
 <211> 157
 <212> PRT
 <213> Artificial

<220>

<223> modif. frag.; BFP F1DX, w. F64L, Y66H mutations, and
posit. 1 Met removed

<400> 553

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 554

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1DX, F64L, Y66H, Y145F mutations

<220>

<221> CDS

<222> (1)..(474)

<400> 554
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggc cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag 474
 Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

<210> 555
 <211> 158
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; BFP F1DX, F64L, Y66H, Y145F mutations

<400> 555
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 556

<211> 471

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1DX, F64L, Y66H, Y145F mutations and posit.1
Met removed

<220>

<221> CDS

<222> (1)..(471)

<400> 556

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60
 ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140
 ttc aac agc cac aac gtc tat atc atg gcc gac aag cag 471
 Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

<210> 557

<211> 157

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F1DX, F64L, Y66H, Y145F mutations and posit.1
Met removed

<400> 557

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 558
<211> 474
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; BFP F1DX with Y145F mutation

<220>
<221> CDS
<222> (1)..(474)

<400> 558
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

100	105	110	
gtg aag ttc gag ggc gac acc ctg	gtg aac cgc atc gag ctg aag ggc		384
Val Lys Phe Glu Gly Asp Thr Leu	Val Asn Arg Ile Glu Leu Lys Gly		
115	120	125	
atc gac ttc aag gag gac ggc aac atc ctg	ggg cac aag ctg gag tac		432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu	Gly His Lys Leu Glu Tyr		
130	135	140	
aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag			474
Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln			
145	150	155	

<210> 559

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F1DX with Y145F mutation

<400> 559

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

<210> 560
 <211> 471
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; BFP F1DX w. Y145F mutation and posit. 1
 Met removed

<220>
 <221> CDS
 <222> (1)..(471)

<400> 560
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30
 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60
 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 gac ttc aag gag gac ggc aac atc ctg ggc cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140
 ttc aac agc cac aac gtc tat atc atg gcc gac aag cag 471
 Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

<210> 561
 <211> 157
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; BFP F1DX w. Y145F mutation and posit. 1
 Met removed

<400> 561

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

<210> 562
 <211> 474
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; BFP F1DX, F46L, F64L, and Y145F mutations

<220>
 <221> CDS
 <222> (1)..(474)

<400> 562

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5					10					15		
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ctg	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Leu	Ile	
			35				40					45				
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55				60						
ctg	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240
Leu	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65					70				75					80		
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85					90					95		
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120					125				
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
130					135					140						
aac	ttc	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag			474
Asn	Phe	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln			
145					150					155						

<210> 563
 <211> 158
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; BFP F1DX, F46L, F64L, and Y145F mutations

<400> 563

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

<210> 564

<211> 471

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1DX, F46L, F64L, and Y145F mutations,
 and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(471)

<400> 564

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
 35 40 45
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60
 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140
 ttc aac agc cac aac gtc tat atc atg gcc gac aag cag 471
 Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

<210> 565
 <211> 157
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; BFP F1DX, F46L, F64L, and Y145F mutations,
 and posit. 1 Met removed

<400> 565

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
 35 40 45
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 566
<211> 474
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; Venus F1DX, with F46L mutation

<220>
<221> CDS
<222> (1)..(474)

<400> 566
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu

	85	90	95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag				336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu				
	100	105	110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc				384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly				
	115	120	125	
atc gac ttc aag gag gac ggc aac atc ctg ggc cac aag ctg gag tac				432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr				
	130	135	140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag				474
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln				
	145	150	155	

<210> 567

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1DX, with F46L mutation

<400> 567

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

<210> 568

<211> 471

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1DX, w. F46L mutation, and posit. 1
 Met removed

<220>

<221> CDS

<222> (1)..(471)

<400> 568

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
 35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag 471

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

<210> 569
 <211> 157
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1DX, w. F46L mutation, and posit. 1
 Met removed

<400> 569

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

<210> 570
 <211> 474
 <212> DNA
 <213> Artificial

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<220>
<223>  modif. frag.; Venus F1DX, w. F46L, F64L mutations

<220>
<221>  CDS
<222>  (1)..(474)

<400>  570
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1          5          10          15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
          20          25          30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
          35          40          45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
          50          55          60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65          70          75          80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
          85          90          95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
          100          105          110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
          115          120          125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
          130          135          140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag      474
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145          150          155

<210>  571
<211>  158
<212>  PRT
<213>  Artificial

<220>
<223>  modif. frag.; Venus F1DX, w. F46L, F64L mutations

<400>  571
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

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1	5	10	15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	20	25	30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile	35	40	45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	50	55	60
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	65	70	75
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	85	90	95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	100	105	110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	115	120	125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	130	135	140
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln	145	150	155

<210> 572
 <211> 471
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1DX, w. F46L, F64L mutations, and
 posit. 1 Met removed

<220>
 <221> CDS
 <222> (1)..(471)

<400> 572	
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60
 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140
 tac aac agc cac aac gtc tat atc atg gcc gac aag cag 471
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

<210> 573
 <211> 157
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1DX, w. F46L, F64L mutations, and
 posit. 1 Met removed

<400> 573

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
 35 40 45
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
145 150 155

<210> 574
<211> 474
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; SEYFP F1DX, w. F64L, M153T mutations

<220>
<221> CDS
<222> (1)..(474)

<400> 574
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

100						105						110						
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384		
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly			
115						120						125						
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432		
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr			
130						135						140						
aac	tac	aac	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag			474		
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln					
145						150						155						

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
 145 150 155

<210> 576

<211> 471

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; SEYFP F1DX, F64L, M153T mutations, and
 position 1 Met removed

<220>

<221> CDS

<222> (1)..(471)

<400> 576

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag 471
 Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
 145 150 155

<210> 577
 <211> 157
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; SEYFP F1DX, F64L, M153T mutations, and
 position 1 Met removed

<400> 577

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
 145 150 155

<210> 578
 <211> 474
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1DX, w. F64L, M153T mutations

<220>
<221> CDS
<222> (1) .. (474)

<400> 578

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5					10					15		

gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			

gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
		35					40					45				

tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55					60					

ctg	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240
Leu	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65					70				75						80	

cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85						90				95			

cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			

gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120					125				

atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130					135					140					

aac	tac	aac	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag			474
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln			
145					150					155						

<210> 579
 <211> 158
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1DX, w. F64L, M153T mutations

<400> 579

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
			20					25					30		

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
 145 150 155

<210> 580
 <211> 471
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1DX, w. F64L, M153T mutations, and
 posit. 1 Met removed

<220>
 <221> CDS
 <222> (1)..(471)

<400> 580
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192

Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu		
50						55					60						
ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240	
Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg		
65					70				75					80			
cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288	
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg		
				85				90					95				
acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336	
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val		
				100				105					110				
aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	384	
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile		
		115					120					125					
gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	432	
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn		
		130				135					140						
tac	aac	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag				471	
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln					
145					150					155							

<210> 581
 <211> 157
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1DX, w. F64L, M153T mutations, and
 posit. 1 Met removed

<400> 581

Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val
1				5					10					15	

Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu
		20					25					30			

Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys
		35					40					45			

Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu
50						55					60				

Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg
65					70					75				80	

His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85

90

95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
 145 150 155

<210> 582

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1DX, F46L, F64L, and M153T mutations

<220>

<221> CDS

<222> (1)..(474)

<400> 582

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
 35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag 474
 Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
 145 150 155

<210> 583

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1DX, F46L, F64L, and M153T mutations

<400> 583

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
 145 150 155

<210> 584

<211> 471

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1DX, F46L, F64L, and M153T mutations,
 and position 1 Met removed

<220>

<221> CDS

<222> (1)..(471)

<400> 584

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
 35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag 471
 Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
 145 150 155

<210> 585
 <211> 157
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1DX, F46L, F64L, and M153T mutations,
 and position 1 Met removed

<400> 585

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
 145 150 155

<210> 586
 <211> 246
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; YFPF2DX, with Met added @ posit. 1

<220>

<221> CDS
<222> (1)..(246)
<223> YFP F2DX corresponds to aa residues 159-239 of YFP

<400> 586
 atg aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag 48
 Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
 1 5 10 15
 gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 96
 Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 20 25 30
 ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag 144
 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
 35 40 45
 tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg 192
 Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 50 55 60
 ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg 240
 Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 65 70 75 80
 tac aag 246
 Tyr Lys

<210> 587
 <211> 82
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; YFPF2DX, with Met added @ posit. 1

<400> 587
 Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
 1 5 10 15
 Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 20 25 30
 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
 35 40 45
 Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 50 55 60
 Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 65 70 75 80
 Tyr Lys

<210> 588
 <211> 243
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; YFPF2DX, with Y203F mutation
 <220>
 <221> CDS
 <222> (1)..(243)

<400> 588
 aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 48
 Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 1 5 10 15
 ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 96
 Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 20 25 30
 gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc ttc cag tcc 144
 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln Ser
 35 40 45
 gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 192
 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 50 55 60
 gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 240
 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 65 70 75 80
 aag 243
 Lys

<210> 589
 <211> 81
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; YFPF2DX, with Y203F mutation

<400> 589

Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 1 5 10 15
 Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 20 25 30
 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln Ser
 35 40 45

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 50 55 60

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 65 70 75 80

Lys

<210> 590
 <211> 246
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; YFP F2DX, w. Y203F mutation and Met added @ posit.
 1

<220>
 <221> CDS
 <222> (1)..(246)

<400> 590
 atg aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag 48
 Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
 1 5 10 15
 gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 96
 Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 20 25 30
 ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc ttc cag 144
 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln
 35 40 45
 tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg 192
 Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 50 55 60
 ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg 240
 Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 65 70 75 80
 tac aag 246
 Tyr Lys

<210> 591
 <211> 82
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; YFP F2DX, w. Y203F mutation and Met added @ posit.
 1

<400> 591

Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
1 5 10 15

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
20 25 30

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln
35 40 45

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
50 55 60

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
65 70 75 80

Tyr Lys

<210> 592

<211> 243

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFPF2DX, with Y203H mutation

<220>

<221> CDS

<222> (1)..(243)

<400> 592

aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 48
Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 96
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc cac cag tcc 144
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser
35 40 45

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 192
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 240
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

aag
Lys

243

<210> 593
<211> 81
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; YFPF2DX, with Y203H mutation

<400> 593

Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser
35 40 45

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

Lys

<210> 594
<211> 246
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; YFP F2DX, w. Y203H mutation and Met added @ posit. 1

<220>
<221> CDS
<222> (1)..(246)

<400> 594

atg aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag 48
Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
1 5 10 15

gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 96
Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
20 25 30

ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc cac cag 144
 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln
 35 40 45
 tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg 192
 Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 50 55 60
 ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg 240
 Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 65 70 75 80
 tac aag 246
 Tyr Lys

<210> 595
 <211> 82
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.;YFP F2DX, w. Y203H mutation and Met added @ posit. 1
 <400> 595

Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
 1 5 10 15

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 20 25 30

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln
 35 40 45

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 50 55 60

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 65 70 75 80

Tyr Lys

<210> 596
 <211> 243
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F2DX, with Y203T mutation
 <220>

<221> CDS

<222> (1)..(243)

<400> 596

aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 48
Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 96
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc act cag tcc 144
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
35 40 45

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 192
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 240
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

aag 243
Lys

<210> 597

<211> 81

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F2DX, with Y203T mutation

<400> 597

Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
35 40 45

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

Lys

<210> 598
 <211> 246
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F2DX, w. Y203T mutation and Met added @ posit.
 1

<220>
 <221> CDS
 <222> (1)..(246)

<400> 598

atg aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag	48
Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu	
1 5 10 15	
gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc	96
Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile	
20 25 30	
ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc act cag	144
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln	
35 40 45	
tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg	192
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu	
50 55 60	
ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg	240
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu	
65 70 75 80	
tac aag	246
Tyr Lys	

<210> 599
 <211> 82
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F2DX, w. Y203T mutation and Met added @ posit.
 1

<400> 599

Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
1 5 10 15
Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
20 25 30
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln

35

40

45

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 50 55 60

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 65 70 75 80

Tyr Lys

<210> 600

<211> 243

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F2DX, w. V163A, Y203T mutations

<220>

<221> CDS

<222> (1)..(243)

<400> 600

aag aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 48
 Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 1 5 10 15

ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 96
 Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 20 25 30

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc 144
 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
 35 40 45

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 192
 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 50 55 60

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 240
 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 65 70 75 80

aag 243
 Lys

<210> 601

<211> 81

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F2DX, w. V163A, Y203T mutations

<400> 601

Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
35 40 45

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

Lys

<210> 602

<211> 246

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F2DX, w. V163A, Y203T mutations and Met
added @ posit. 1

<220>

<221> CDS

<222> (1)..(246)

<400> 602

atg aag aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag 48
Met Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu
1 5 10 15

gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 96
Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
20 25 30

ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag 144
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
35 40 45

tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg 192
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
50 55 60

ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg 240
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
65 70 75 80

tac aag
Tyr Lys

246

<210> 603
<211> 82
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; CFP F2DX, w. V163A, Y203T mutations and Met
added @ posit. 1

<400> 603

Met Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu
1 5 10 15

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
20 25 30

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
35 40 45

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
50 55 60

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
65 70 75 80

Tyr Lys

<210> 604
<211> 246
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; Venus F2DX, with S175G mutation

<220>
<221> CDS
<222> (1)..(246)

<400> 604

atg aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag 48
Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
1 5 10 15

gac ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 96
Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile

20

25

30

ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag	144
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln	
35 40 45	
tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg	192
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu	
50 55 60	
ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg	240
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu	
65 70 75 80	
tac aag	246
Tyr Lys	

<210> 605
 <211> 82
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F2DX, with S175G mutation
 <400> 605

Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu	
1 5 10 15	
Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile	
20 25 30	
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln	
35 40 45	
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu	
50 55 60	
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu	
65 70 75 80	
Tyr Lys	

<210> 606
 <211> 246
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; Venus F2DX, w. S175G mutation and Met
 added @ posit. 1

<220>
 <221> CDS
 <222> (1)..(246)

 <400> 606
 atg aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag 48
 Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
 1 5 10 15

 gac ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 96
 Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 20 25 30

 ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag 144
 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
 35 40 45

 tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg 192
 Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 50 55 60

 ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg 240
 Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 65 70 75 80

 tac aag 246
 Tyr Lys

<210> 607
 <211> 82
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F2DX, w. S175G mutation and Met
 added @ posit. 1

<400> 607

 Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
 1 5 10 15

 Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 20 25 30

 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
 35 40 45

 Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 50 55 60

 Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 65 70 75 80

Tyr Lys

<210> 608
 <211> 243
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; Venus F2DX, w. V163A, S175G mutations

<220>
 <221> CDS
 <222> (1)..(243)

<400> 608
 aag aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 48
 Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 1 5 10 15
 ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 96
 Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 20 25 30
 gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc 144
 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
 35 40 45
 gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 192
 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 50 55 60
 gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 240
 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 65 70 75 80
 aag 243
 Lys

<210> 609
 <211> 81
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F2DX, w. V163A, S175G mutations

<400> 609

Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 1 5 10 15
 Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 20 25 30

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
 35 40 45

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 50 55 60

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 65 70 75 80

Lys

<210> 610

<211> 246

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F2DX, w. V163A, S175G mutations and Met
 added @ posit. 1

<220>

<221> CDS

<222> (1)..(246)

<400> 610

atg aag aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag 48
 Met Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu
 1 5 10 15

gac ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 96
 Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 20 25 30

ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag 144
 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
 35 40 45

tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg 192
 Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 50 55 60

ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg 240
 Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 65 70 75 80

tac aag 246
 Tyr Lys

<210> 611

<211> 82

<212> PRT

<213> Artificial

<220>
 <223> modif. frag.; Venus F2DX, w. V163A, S175G mutations and Met added @ posit. 1

<400> 611

Met Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu
 1 5 10 15

Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 20 25 30

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
 35 40 45

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 50 55 60

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 65 70 75 80

Tyr Lys

<210> 612
 <211> 474
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; YFP F1D with position 1 Met removed

<220>
 <221> CDS
 <222> (1)..(474)
 <223> YFP F1D corresponds to aa residues 1-159 of YFP

<400> 612

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe

50	55	60	
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg			240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg			
65	70	75	80
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc			288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg			
	85	90	95
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg			336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val			
	100	105	110
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc			384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile			
	115	120	125
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac			432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn			
	130	135	140
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag			474
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys			
145	150	155	
<210> 613			
<211> 158			
<212> PRT			
<213> Artificial			
<220>			
<223> modif. frag.; YFP F1D with position 1 Met removed			
<400> 613			
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val			
1	5	10	15
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu			
	20	25	30
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys			
	35	40	45
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe			
	50	55	60
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg			
65	70	75	80
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg			
	85	90	95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 614

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1D with K79R mutation

<220>

<221> CDS

<222> (1)..(477)

<400> 614

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly

115

120

125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag 477
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 615
 <211> 159
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; YFP F1D with K79R mutation

<400> 615

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 616
 <211> 474
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; YFP F1D w. K79R mutation, Met @ posit. 1 removed
 <220>
 <221> CDS
 <222> (1)..(474)

<400> 616

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	474
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
145 150 155	

<210> 617
 <211> 158
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; YFP F1D w. K79R mutation, Met @ posit. 1 removed

<400> 617

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 618

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1D with Y66F mutation

<220>

<221> CDS

<222> (1)..(477)

<400> 618

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

48

1	5	10	15	
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc				96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	20	25	30	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc				144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	35	40	45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc				192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	50	55	60	
ttc ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag				240
Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	65	70	75	80
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag				288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	85	90	95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag				336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	100	105	110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc				384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	115	120	125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac				432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	130	135	140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag				477
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	145	150	155	

<210> 619

<211> 159

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1D with Y66F mutation

<400> 619

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 620

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1D w. Y66F mutation, Met @ posit. 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 620

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg

65

70

75

80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140
 tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag 474
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 621
 <211> 158
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; YFP F1D w. Y66F mutation, Met @ posit. 1 removed

<400> 621

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60
 Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 622
<211> 477
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; YFP F1D with Q69K mutation

<220>
<221> CDS
<222> (1)..(477)

<400> 622
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60
ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr

130	135	140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag			477
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys			
145	150	155	

<210> 623
 <211> 159
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; YFP F1D with Q69K mutation

<400> 623

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
			20					25					30		

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
		35					40					45			

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
	50					55					60				

Phe	Gly	Tyr	Gly	Leu	Lys	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys
65					70					75				80	

Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
			85						90					95	

Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
		100						105					110		

Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
		115					120					125			

Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr
	130					135					140				

Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	
145					150					155					

<210> 624
 <211> 474
 <212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1D w. Q69K mutation, Met @ posit. 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 624

gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc	48
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
1			5						10					15		

gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag	96
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
			20				25						30			

ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	144
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
		35					40					45				

acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ttc	192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	
	50					55					60					

ggc	tac	ggc	ctg	aag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240
Gly	Tyr	Gly	Leu	Lys	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
65					70				75						80	

cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
				85					90					95		

acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
			100					105					110			

aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	384
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
		115					120					125				

gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
		130				135					140					

tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag			474
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys			
145					150					155						

<210> 625

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1D w. Q69K mutation, Met @ posit. 1 removed

<400> 625

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 626

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; citrine F1D w. V68L, Q69M mutations

<220>

<221> CDS

<222> (1)..(477)

<400> 626

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

20

25

30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ttc ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag	240
Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	477
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
145 150 155	

<210> 627
 <211> 159
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; citrine F1D w. V68L, Q69M mutations

<400> 627

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	

Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 628

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; citrine F1D w. V68L, Q69M mutations, Met @
posit.1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 628

gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc	48
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
1			5						10					15		

gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag	96
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
			20					25					30			

ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	144
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
			35				40					45				

acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ttc	192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	
			50			55					60					

ggc	tac	ggc	ctg	atg	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240
Gly	Tyr	Gly	Leu	Met	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
65					70					75					80	

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

gac ttc aag gag gac ggc aac atc ctg ggc cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag 474
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 629

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; citrine F1D w. V68L, Q69M mutations, Met @
 posit.1 removed

<400> 629

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 630
 <211> 477
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1D with F64L mutation

<220>
 <221> CDS
 <222> (1)..(477)

<400> 630
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr

130 135 140
 aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag 477
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

 <210> 631
 <211> 159
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; CFP F1D with F64L mutation

 <400> 631

 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

 <210> 632
 <211> 474
 <212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D with F64L mutation, Met @ posit. 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 632

gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc	48
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
1			5					10					15			

gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag	96
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
		20					25					30				

ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	144
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
		35					40				45					

acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ctg	192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	
	50					55				60						

ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240
Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
65				70				75						80		

cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
				85				90					95			

acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
			100				105						110			

aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	384
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
		115				120						125				

gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
	130					135					140					

tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag			474
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys			
145					150					155						

<210> 633

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1D with F64L mutation, Met @ posit. 1 removed

<400> 633

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 634
<211> 477
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; YFP F1D with F46L mutation

<220>
<221> CDS
<222> (1)..(477)

<400> 634
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

20										25					30					
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ctg	atc	144				
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Leu	Ile					
35						40						45								
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192				
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr					
50						55						60								
ttc	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240				
Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys					
65						70						75			80					
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288				
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu					
			85						90						95					
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336				
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu					
			100						105						110					
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384				
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly					
			115						120						125					
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432				
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr					
130						135						140								
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag		477				
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys						
145			150						155											

<210> 635

<211> 159

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1D with F46L mutation

<400> 635

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
			20					25					30		

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Leu	Ile
		35					40					45			

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
	50						55				60				

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 636

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1D with F46L mutation, Met @ posit. 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 636

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val

100										105					110					
aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc		384			
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile					
		115					120					125								
gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac		432			
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn					
		130				135					140									
tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag				474			
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys							
145					150					155										

<210> 637
 <211> 158
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; YFP F1D with F46L mutation, Met @ posit. 1 removed

<400> 637

Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val
1				5					10					15	

Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu
		20					25					30			

Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Leu	Ile	Cys
		35				40					45				

Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe
	50					55					60				

Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg
65					70				75					80	

His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg
				85					90					95	

Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val
			100					105						110	

Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile
		115					120					125			

Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn
		130				135					140				

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 638
 <211> 477
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; YFP F1D with F46L, F64L mutations

<220>
 <221> CDS
 <222> (1)..(477)

<400> 638
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
 35 40 45
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag 477
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 639
 <211> 159
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; YFP F1D with F46L, F64L mutations

<400> 639

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 640
 <211> 474
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; YFP F1D w. F46L, F64L mutations, and
 Met @ posit. 1 removed

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<220>
<221> CDS
<222> (1)..(474)

<400> 640
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1          5          10          15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
          20          25          30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
          35          40          45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
          50          55          60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65          70          75          80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
          85          90          95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
          100          105          110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
          115          120          125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
          130          135          140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag      474
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145          150          155

<210> 641
<211> 158
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; YFP F1D w. F46L, F64L mutations, and
      Met @ posit. 1 removed

<400> 641
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1          5          10          15

```


Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 642
 <211> 477
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1D with F64L, M153T mutations

<220>
 <221> CDS
 <222> (1)..(477)

<400> 642
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile

35	40	45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc			192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
50	55	60	
ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag			240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys			
65	70	75	80
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag			288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
85	90	95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag			336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
100	105	110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc			384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
115	120	125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac			432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130	135	140	
aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag			477
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys			
145	150	155	

<210> 643

<211> 159

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1D with F64L, M153T mutations

<400> 643

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

<210> 644

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1D w. F64L, M153T mutations, and
Met @ posit. 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 644

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val

100	105	110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc			384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile			
115	120	125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac			432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn			
130	135	140	
tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag			474
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys			
145	150	155	

<210> 645
 <211> 158
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1D w. F64L, M153T mutations, and
 Met @ posit. 1 removed

<400> 645

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
 145 150 155

<210> 646
 <211> 477
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1D with F46L, M153T mutations

<220>
 <221> CDS
 <222> (1)..(477)

<400> 646
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
 35 40 45
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag 477
 Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
 145 150 155

<210> 647
 <211> 159
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1D with F46L, M153T mutations
 <400> 647

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
 145 150 155

<210> 648
 <211> 474
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1D w. F46L, M153T mutations, and
 Met @ posit. 1 removed

<220>
 <221> CDS
 <222> (1)..(474)

 <400> 648
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
 35 40 45

 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

 tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag 474
 Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
 145 150 155

 <210> 649
 <211> 158
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; Venus F1D w. F46L, M153T mutations, and
 Met @ posit. 1 removed

 <400> 649
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
 145 150 155

<210> 650
 <211> 477
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1D, F46L, F64L, and M153T mutations
 <220>
 <221> CDS
 <222> (1)..(477)

<400> 650
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile	
35 40 45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Arg His Asp Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag	477
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys	
145 150 155	

<210> 651

<211> 159

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1D, F46L, F64L, and M153T mutations

<400> 651

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

<210> 652

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1D, F46L, F64L, and M153T mutations,
Met @ position 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 652

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag	474
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys	
145 150 155	

<210> 653
 <211> 158
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1D, F46L, F64L, and M153T mutations,
 Met @ position 1 removed

<400> 653

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys	
35 40 45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
50 55 60	
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
 145 150 155

<210> 654
 <211> 477
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1D w. F46L, F64L, N146I mutations

<220>
 <221> CDS
 <222> (1)..(477)

<400> 654
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
 35 40 45
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr

130 135 140
 aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag 477
 Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

 <210> 655
 <211> 159
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; CFP F1D w. F46L, F64L, N146I mutations

 <400> 655

 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
 35 40 45

 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

 Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

 <210> 656
 <211> 474

<212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1D, w. F46L, F64L, N146I mutations,
 Met @ position 1 removed

<220>
 <221> CDS
 <222> (1)..(474)

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<400> 656
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1          5          10          15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
          20          25          30

gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
          35          40          45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
          50          55          60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65          70          75          80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
          85          90          95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
          100          105          110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
          115          120          125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
          130          135          140

tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag      474
Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145          150          155

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<210> 657
 <211> 158
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1D, w. F46L, F64L, N146I mutations,

Met @ position 1 removed

<400> 657

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 658

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D, w. F64L, S65T, and Y66W mutations

<220>

<221> CDS

<222> (1)..(477)

<400> 658

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ctg acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	477
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
145 150 155	

<210> 659

<211> 159

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1D, w. F64L, S65T, and Y66W mutations

<400> 659

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 660

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D, w. F64L, S65T, and Y66W mutations, and
Met @ position 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 660

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240

Thr	Trp	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
65					70					75					80	
cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
				85					90					95		
acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
			100					105					110			
aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	384
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
		115					120					125				
gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
		130				135					140					
tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag			474
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys			
145					150					155						

<210> 661
 <211> 158
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; CFP F1D, w. F64L, S65T, and Y66W mutations, and
 Met @ position 1 removed

 <400> 661

Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
1				5					10					15		
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
		20						25					30			
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
		35					40					45				
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	
	50					55					60					
Thr	Trp	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
65					70					75					80	
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
				85					90					95		
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	

100

105

110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 662
<211> 477
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; CFP F1D with Y66W mutation

<220>
<221> CDS
<222> (1)..(477)

<400> 662
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60
ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr

130 135 140
 aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag 477
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

 <210> 663
 <211> 159
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; CFP F1D with Y66W mutation

 <400> 663

 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

 Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

 <210> 664
 <211> 474
 <212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D with Y66W mutation, Met @ posit. 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 664

gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc	48
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
1			5					10					15			

gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag	96
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
		20					25					30				

ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	144
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
		35					40					45				

acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ttc	192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	
	50					55					60					

ggc	tgg	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240
Gly	Trp	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
65				70					75					80		

cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
				85				90						95		

acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
			100					105					110			

aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	384
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
		115					120					125				

gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
		130				135					140					

tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag			474
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys			
145					150					155						

<210> 665

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1D with Y66W mutation, Met @ posit. 1 removed

<400> 665

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 666
<211> 477
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; CFP F1D with Y66W, N146I mutations

<220>
<221> CDS
<222> (1)..(477)

<400> 666
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

20

25

30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag	477
Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
145 150 155	

<210> 667

<211> 159

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1D with Y66W, N146I mutations

<400> 667

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 668

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D w. Y66W, N146I mutations, and
Met @ posit. 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 668

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

gac ttc aag gag gac ggc aac atc ctg ggc cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag 474
 Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 669

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1D w. Y66W, N146I mutations, and
 Met @ posit. 1 removed

<400> 669

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 670
 <211> 477
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1D with Y66W, M153T mutations

<220>
 <221> CDS
 <222> (1)..(477)

<400> 670
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr

130 135 140
 aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag 477
 Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
 145 150 155

 <210> 671
 <211> 159
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; CFP F1D with Y66W, M153T mutations

 <400> 671

 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

 Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

 Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
 145 150 155

 <210> 672
 <211> 474
 <212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D, w. Y66W and M153T mutations, and
Met @ position 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 672

gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc	48
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
1			5					10					15			

gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag	96
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
		20					25					30				

ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	144
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
		35					40					45				

acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ttc	192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	
		50				55					60					

ggc	tgg	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240
Gly	Trp	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
65				70				75						80		

cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
				85				90						95		

acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
			100				105						110			

aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	384
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
		115				120						125				

gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
		130				135					140					

tac	aac	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag	aag			474
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys			
145					150					155						

<210> 673

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1D, w. Y66W and M153T mutations, and

Met @ position 1 removed

<400> 673

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

<210> 674

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D with N146I mutation

<220>

<221> CDS

<222> (1)..(477)

<400> 674

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag	477
Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
145 150 155	

<210> 675

<211> 159

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1D with N146I mutation

<400> 675

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 676

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D w. N146I mutation, Met @ posit. 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 676

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg

65	70	75	80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc				288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg				
	85	90	95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg				336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val				
	100	105	110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc				384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile				
	115	120	125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac				432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn				
	130	135	140	
tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag				474
Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys				
	145	150	155	

<210> 677

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1D w. N146I mutation, Met @ posit. 1 removed

<400> 677

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 678
 <211> 477
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1D with M153T mutation

<220>
 <221> CDS
 <222> (1)..(477)

<400> 678
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr

130 135 140
 aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag 477
 Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
 145 150 155

 <210> 679
 <211> 159
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; CFP F1D with M153T mutation

 <400> 679

 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

 Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
 145 150 155

 <210> 680
 <211> 474
 <212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D w. M153T mutation, Met @ posit. 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 680

gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc	48
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
1			5						10					15		

gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag	96
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
			20				25						30			

ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	144
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
		35					40					45				

acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ttc	192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	
	50					55					60					

ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240
Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
65				70					75						80	

cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
				85				90						95		

acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
			100					105					110			

aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	384
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
		115					120					125				

gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
		130				135					140					

tac	aac	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag	aag			474
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys			
145					150					155						

<210> 681

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1D w. M153T mutation, Met @ posit. 1 removed

<400> 681

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

<210> 682
<211> 477
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; CFP F1D with N146I, M153T mutations

<220>
<221> CDS
<222> (1)..(477)

<400> 682
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

20

25

30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag	477
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys	
145 150 155	

<210> 683

<211> 159

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1D with N146I, M153T mutations

<400> 683

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

<210> 684
<211> 474
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; CFP F1D w. N146I, M153T mutations, and
Met @ posit. 1 removed

<220>
<221> CDS
<222> (1)..(474)

<400> 684
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag 474
 Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
 145 150 155

<210> 685
 <211> 158
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1D w. N146I, M153T mutations, and
 Met @ posit. 1 removed

<400> 685

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
 145 150 155

<210> 686

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D, w. Y66W, N146I, and M153T mutations

<220>

<221> CDS

<222> (1)..(477)

<400> 686

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag
 Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
 145 150 155

477

<210> 687

<211> 159

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1D, w. Y66W, N146I, and M153T mutations

<400> 687

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
 145 150 155

<210> 688

<211> 474

<212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1D, Y66W, N146I, and M153T mutations,
 Met @ posit. 1 removed

<220>
 <221> CDS
 <222> (1)..(474)

<400> 688

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag	474
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys	
145 150 155	

<210> 689
 <211> 158
 <212> PRT
 <213> Artificial

<220>

<223> modif. frag.; CFP F1D, Y66W, N146I, and M153T mutations,
Met @ posit. 1 removed

<400> 689

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys
145 150 155

<210> 690

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D with S65A mutation

<220>

<221> CDS

<222> (1)..(477)

<400> 690

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

48

1	5	10	15	
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc				96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	20	25	30	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc				144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	35	40	45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc				192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	50	55	60	
ttc gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag				240
Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	65	70	75	80
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag				288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	85	90	95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag				336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	100	105	110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc				384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	115	120	125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac				432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	130	135	140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag				477
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	145	150	155	

<210> 691

<211> 159

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1D with S65A mutation

<400> 691

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 692

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D w. S65A mutation, Met @ posit. 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 692

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

	85	90	95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg				336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val				
	100	105	110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc				384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile				
	115	120	125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac				432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn				
	130	135	140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag				474
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys				
	145	150	155	

<210> 693

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1D w. S65A mutation, Met @ posit. 1 removed

<400> 693

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 694

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1D, w. S65A, Y66W, and S72A mutations

<220>

<221> CDS

<222> (1)..(477)

<400> 694

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

477

<210> 695
 <211> 159
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1D, w. S65A, Y66W, and S72A mutations

<400> 695

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 696
 <211> 474
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1D,S65A, Y66W, and S72A mutations,
 Met @ posit. 1 removed

<220>
 <221> CDS
 <222> (1)..(474)

<400> 696

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
 gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
 tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	474
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
145 150 155	

<210> 697
 <211> 158
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1D,S65A, Y66W, and S72A mutations,
 Met @ posit. 1 removed

<400> 697

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 698

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1D with Y66H mutation

<220>

<221> CDS

<222> (1)..(477)

<400> 698

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30.	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ttc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag	477
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
145 150 155	

<210> 699

<211> 159

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F1D with Y66H mutation

<400> 699

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr

50

55

60

Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 700

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1D w. Y66H mutation, Met @ posit. 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 700

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg

	85	90	95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg				336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val				
	100	105	110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc				384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile				
	115	120	125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac				432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn				
	130	135	140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag				474
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys				
	145	150	155	

<210> 701

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F1D w. Y66H mutation, Met @ posit. 1 removed

<400> 701

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 702

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1D w. F64L, Y66H mutations

<220>

<221> CDS

<222> (1)..(477)

<400> 702

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag 477
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys

145

150

155

<210> 703

<211> 159

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F1D w. F64L, Y66H mutations

<400> 703

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 704

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1D w. F64L, Y66H mutations, and

Met @ posit. 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 704

gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc	48
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
1			5					10						15		

gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag	96
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
		20					25					30				

ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	144
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
		35					40					45				

acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ctc	192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu	
	50					55					60					

ggc	cac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240
Gly	His	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
65				70				75						80		

cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
				85				90						95		

acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
			100				105						110			

aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	384
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
		115				120						125				

gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
	130				135						140					

tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag			474
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys			
145				150				155								

<210> 705

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F1D w. F64L, Y66H mutations, and
Met @ posit. 1 removed

<400> 705

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val

1	5	10	15
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	20	25	30
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	35	40	45
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	50	55	60
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	65	70	75
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	85	90	95
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	100	105	110
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	115	120	125
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	130	135	140
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	145	150	155

<210> 706

<211> 477

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1D, w. F64L, Y66H, and Y145F mutations

<220>

<221> CDS

<222> (1)..(477)

<400> 706

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag	477
Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
145 150 155	

<210> 707

<211> 159

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F1D, w. F64L, Y66H, and Y145F mutations

<400> 707

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys

65		70		75		80									
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
			85						90					95	

Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
		100						105					110		

Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
		115					120					125			

Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr
	130					135					140				

Asn	Phe	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys
145					150					155				

<210> 708
 <211> 474
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; BFP F1D, w. F64L, Y66H, and Y145F mutations,
 Met @ posit. 1 removed

<220>
 <221> CDS
 <222> (1)..(474)

<400>	708	
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc		48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val		
1 5 10 15		
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag		96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu		
20 25 30		
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc		144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys		
35 40 45		
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc		192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu		
50 55 60		
ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg		240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg		
65 70 75 80		
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc		288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg		
85 90 95		

acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
			100					105					110			

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag 474
 Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 709

<211> 158

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F1D, w. F64L, Y66H, and Y145F mutations,
 Met @ posit. 1 removed

<400> 709

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 710
 <211> 477
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; BFP F1D, with Y145F mutation

<220>
 <221> CDS
 <222> (1)..(477)

<400> 710
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag 477
 Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 711

<211> 159
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; BFP F1D, with Y145F mutation

<400> 711

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 712
<211> 474
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; BFP F1D, w. Y145F mutation, Met @ posit. 1 removed

<220>
<221> CDS
<222> (1)..(474)

<400> 712

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag	474
Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys	
145 150 155	

<210> 713
 <211> 158
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; BFP FlD, w. Y145F mutation, Met @ posit. 1 removed

<400> 713

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 714
 <211> 477
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; BFP F1D, w. F46L, F64L, and Y145F mutations
 <220>
 <221> CDS
 <222> (1)..(477)

<400> 714
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
 35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
50						55					60						
ctg	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240	
Leu	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys		
65				70					75					80			
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288	
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		
			85					90					95				
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336	
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		
			100					105					110				
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384	
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly		
		115					120					125					
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432	
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		
	130					135					140						
aac	ttc	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag		477	
Asn	Phe	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys			
145					150					155							

<210> 715

<211> 159

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F1D, w. F46L, F64L, and Y145F mutations

<400> 715

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1			5					10						15	

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
		20					25					30			

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Leu	Ile
	35					40					45				

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
50					55						60				

Leu	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys
65				70					75					80	

Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
			85					90					95		

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
145 150 155

<210> 716

<211> 474

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1D, w. F46L, F64L, and Y145F mutations,
Met @ posit. 1 removed

<220>

<221> CDS

<222> (1)..(474)

<400> 716

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag 474
 Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 717
 <211> 158
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; BFP F1D, w. F46L, F64L, and Y145F mutations,
 Met @ posit. 1 removed

<400> 717

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 145 150 155

<210> 718
 <211> 243
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; YFP F2D, w. Met added @ posit. 1

<220>
 <221> CDS
 <222> (1)..(243)
 <223> YFP F2D corresponds to aa residues 159-239 of YFP

<400> 718
 atg aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 48
 Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 1 5 10 15
 ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 96
 Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 20 25 30
 gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc 144
 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
 35 40 45
 gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 192
 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 50 55 60
 gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 240
 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 65 70 75 80
 aag 243
 Lys

<210> 719
 <211> 81
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; YFP F2D, w. Met added @ posit. 1

<400> 719

Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 1 5 10 15

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly

20

25

30

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
 35 40 45

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 50 55 60

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 65 70 75 80

Lys

<210> 720

<211> 240

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F2D, with Y203F mutation

<220>

<221> CDS

<222> (1)..(240)

<400> 720

aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc 48
 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
 1 5 10 15

agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 96
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 20 25 30

ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc gcc 144
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala
 35 40 45

ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag 192
 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 50 55 60

ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag 240
 Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 65 70 75 80

<210> 721

<211> 80

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F2D, with Y203F mutation

<400> 721

Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
1 5 10 15

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
20 25 30

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala
35 40 45

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
50 55 60

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
65 70 75 80

<210> 722

<211> 243

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F2D, w. Y203F mutation, Met added @ posit. 1

<220>

<221> CDS

<222> (1)..(243)

<400> 722

atg aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 48
Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 96
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc 144
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
35 40 45

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 192
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 240
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

aag 243
Lys

<210> 723
 <211> 81
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; YFP F2D, w. Y203F mutation, Met added @ posit. 1

<400> 723

Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 1 5 10 15

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 20 25 30

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
 35 40 45

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 50 55 60

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 65 70 75 80

Lys

<210> 724
 <211> 240
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; YFP F2D, with Y203H mutation

<220>
 <221> CDS
 <222> (1)..(240)

<400> 724

aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc 48
 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
 1 5 10 15

agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 96
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 20 25 30

ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc cac cag tcc gcc 144
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser Ala
 35 40 45

ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag	192
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu	
50 55 60	

ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag	240
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	
65 70 75 80	

<210> 725
 <211> 80
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; YFP F2D, with Y203H mutation

<400> 725

Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
1 5 10 15

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
20 25 30

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser Ala
35 40 45

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
50 55 60

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
65 70 75 80

<210> 726
 <211> 243
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; YFP F2D, w. Y203H mutation, Met added @ posit. 1

<220>
 <221> CDS
 <222> (1)..(243)

<400> 726

atg aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	48
Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
1 5 10 15	

ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc	96
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly	
20 25 30	

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc cac cag tcc 144
 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser
 35 40 45

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 192
 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 50 55 60

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 240
 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 65 70 75 80

aag 243
 Lys

<210> 727
 <211> 81
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; YFP F2D, w. Y203H mutation, Met added @ posit. 1
 <400> 727

Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 1 5 10 15

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 20 25 30

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser
 35 40 45

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 50 55 60

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 65 70 75 80

Lys

<210> 728
 <211> 240
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F2D, with Y203T mutation

<220>
 <221> CDS
 <222> (1)..(240)

 <400> 728
 aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc 48
 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
 1 5 10 15
 agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 96
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 20 25 30
 ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc 144
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
 35 40 45
 ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag 192
 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 50 55 60
 ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag 240
 Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 65 70 75 80

 <210> 729
 <211> 80
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; CFP F2D, with Y203T mutation

 <400> 729
 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
 1 5 10 15
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 20 25 30
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
 35 40 45
 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 50 55 60
 Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 65 70 75 80

 <210> 730
 <211> 243
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F2D, w. Y203T mutation, Met added @ posit. 1

<220>
 <221> CDS
 <222> (1)..(243)

<400> 730

atg aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	48
Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
1 5 10 15	
ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc	96
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly	
20 25 30	
gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc	144
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser	
35 40 45	
gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg	192
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu	
50 55 60	
gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac	240
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr	
65 70 75 80	
aag	243
Lys	

<210> 731
 <211> 81
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F2D, w. Y203T mutation, Met added @ posit. 1

<400> 731

Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
1 5 10 15	
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly	
20 25 30	
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser	
35 40 45	
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu	
50 55 60	

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

Lys

<210> 732

<211> 240

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F2D, w. V163A, Y203T mutations

<220>

<221> CDS

<222> (1)..(240)

<400> 732

aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc 48
Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
1 5 10 15

agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 96
Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
20 25 30

ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc 144
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
35 40 45

ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag 192
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
50 55 60

ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag 240
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
65 70 75 80

<210> 733

<211> 80

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F2D, w. V163A, Y203T mutations

<400> 733

Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
1 5 10 15

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
20 25 30

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
 35 40 45

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 50 55 60

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 65 70 75 80

<210> 734
 <211> 243
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag. CFP F2D, w. V163A, Y203T, Met added @ posit. 1

<220>
 <221> CDS
 <222> (1)..(243)

<400> 734
 atg aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 48
 Met Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 1 5 10 15
 ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 96
 Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 20 25 30
 gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc 144
 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
 35 40 45
 gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 192
 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 50 55 60
 gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 240
 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 65 70 75 80
 aag 243
 Lys

<210> 735
 <211> 81
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag. CFP F2D, w. V163A, Y203T, Met added @ posit. 1

<400> 735

Met Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 20 25 30

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
 35 40 45

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 50 55 60

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 65 70 75 80

Lys

<210> 736
 <211> 240
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; Venus F2D, with S175G mutation

<220>
 <221> CDS
 <222> (1)..(240)

<400> 736
 aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc 48
 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
 1 5 10 15
 ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 96
 Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 20 25 30
 ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc gcc 144
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala
 35 40 45
 ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag 192
 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 50 55 60
 ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag 240
 Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 65 70 75 80

<210> 737
 <211> 80
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F2D, with S175G mutation
 <400> 737

Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
 1 5 10 15

Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 20 25 30

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala
 35 40 45

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 50 55 60

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 65 70 75 80

<210> 738
 <211> 243
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; Venus F2D, w. S175G mutation, and Met added
 @ posit. 1

<220>
 <221> CDS
 <222> (1)..(243)

<400> 738

atg aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	48
Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
1 5 10 15	
ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc	96
Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly	
20 25 30	
gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc	144
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser	
35 40 45	
gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg	192
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu	
50 55 60	
gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac	240
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr	
65 70 75 80	
aag	243

Lys

<210> 739

<211> 81

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F2D, w. S175G mutation, and Met added
@ posit. 1

<400> 739

Met Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
35 40 45

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

Lys

<210> 740

<211> 240

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F2D, w. V163A, S175G mutations

<220>

<221> CDS

<222> (1)..(240)

<400> 740

aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc 48
Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
1 5 10 15

ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 96
Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
20 25 30

ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc gcc 144
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala
 35 40 45

ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag 192
 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 50 55 60

ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag 240
 Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 65 70 75 80

<210> 741
 <211> 80
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F2D, w. V163A, S175G mutations

<400> 741

Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
 1 5 10 15

Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 20 25 30

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala
 35 40 45

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 50 55 60

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 65 70 75 80

<210> 742
 <211> 243
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag. Venus F2D, w. V163A, S175G, and Met added
 @ posit. 1

<220>
 <221> CDS
 <222> (1)..(243)

<400> 742
 atg aac ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 48
 Met Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 1 5 10 15

<213> Artificial

<220>

<223> modif. frag.; YFP F1E, with position 1 Met removed

<220>

<221> CDS

<222> (1)..(519)

<223> YFP F1E corresponds to aa residues 1-174 of YFP

<400> 744

gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc	48
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
1			5						10					15		

gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag	96
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
		20					25						30			

ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	144
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
		35					40					45				

acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ttc	192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	
	50					55					60					

ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240
Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
65				70					75					80		

cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
			85					90					95			

acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
			100					105					110			

aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	384
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
		115				120						125				

gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
	130					135					140					

tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	ggc	480
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	
145					150				155						160	

atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac				519
Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp				
			165						170							

<210> 745

<211> 173

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1E, with position 1 Met removed

<400> 745

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 746

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1E, with K79R mutation

<220>

<221> CDS

<222> (1)..(522)

<400> 746

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5					10					15		

gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			

gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
		35					40					45				

tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55					60					

ttc	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	cgc	240
Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Arg	
65					70				75						80	

cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85						90					95		

cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			

gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120					125				

atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130					135					140					

aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
145					150					155					160	

ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac			522
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp			
			165					170								

<210> 747
 <211> 174
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; YFP F1E, with K79R mutation

<400> 747

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 748

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1E, with K79R mutation, and posit. 1
 Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 748

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96

Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu		
			20					25						30			
ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc		144
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys		
		35					40					45					
acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ttc		192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe		
	50					55					60						
ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	cgc	cgg		240
Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Arg	Arg		
65				70				75						80			
cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc		288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg		
				85				90						95			
acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg		336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val		
			100				105						110				
aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc		384
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile		
		115				120						125					
gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac		432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn		
	130				135						140						
tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	ggc		480
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly		
145				150				155						160			
atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac					519
Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp					
			165					170									

<210> 749
 <211> 173
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; YFP F1E, with K79R mutation, and posit. 1
 Met removed

<400> 749

Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val		
1			5						10					15			

Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu		
			20					25						30			

Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys		
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--	--

35	40	45
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe		
50	55	60
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg		
65	70	75
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg		
	85	90
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val		
	100	105
		110
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile		
	115	120
		125
Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn		
	130	135
		140
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly		
145	150	155
		160
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp		
	165	170

<210> 750
 <211> 522
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; YFP F1E, with Y66F mutation

<220>
 <221> CDS
 <222> (1)..(522)

<400> 750	
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
145 150 155 160	
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
165 170	

<210> 751

<211> 174

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1E, with Y66F mutation

<400> 751

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 752

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1E, with Y66F mutation, and posit. 1
Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 752

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

gac ttc aag gag gac ggc aac atc ctg ggc cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 519
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 753
 <211> 173
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; YFP F1E, with Y66F mutation, and posit. 1
 Met removed

<400> 753

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 754
 <211> 522
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; YFP F1E, with Q69K mutation

<220>
 <221> CDS
 <222> (1)..(522)

<400> 754
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

100	105	110	
gtg aag ttc gag ggc gac acc ctg	gtg aac cgc atc gag ctg aag ggc		384
Val Lys Phe Glu Gly Asp Thr Leu	Val Asn Arg Ile Glu Leu Lys Gly		
115	120	125	
atc gac ttc aag gag gac ggc aac atc	ctg ggg cac aag ctg gag tac		432
Ile Asp Phe Lys Glu Asp Gly Asn Ile	Leu Gly His Lys Leu Glu Tyr		
130	135	140	
aac tac aac agc cac aac gtc tat atc	atg gcc gac aag cag aag aac		480
Asn Tyr Asn Ser His Asn Val Tyr Ile	Met Ala Asp Lys Gln Lys Asn		
145	150	155	160
ggc atc aag gtg aac ttc aag atc cgc	cac aac atc gag gac		522
Gly Ile Lys Val Asn Phe Lys Ile Arg	His Asn Ile Glu Asp		
165	170		

<210> 755

<211> 174

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1E, with Q69K mutation

<400> 755

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 756
 <211> 519
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; YFP F1E, with Q69K mutation, and posit. 1
 Met removed

<220>
 <221> CDS
 <222> (1)..(519)

<400> 756
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30
 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60
 ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 758
<211> 522
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; citrine F1E, w. V68L, Q69M mutations

<220>
<221> CDS
<222> (1)..(522)

<400> 758
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60
ttc ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp

165

170

<210> 759
 <211> 174
 <212> PRT
 <213> Artificial

<220>

<223> modif. frag.; citrine F1E, w. V68L, Q69M mutations

<400> 759

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 760
 <211> 519
 <212> DNA

<213> Artificial

<220>

<223> modif. frag.; citrine F1E, w. V68L, Q69M mutations, and
posit.1 Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 760

gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc	48
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
1			5					10					15			

gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag	96
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
		20					25					30				

ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	144
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
		35					40					45				

acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ttc	192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	
	50					55					60					

ggc	tac	ggc	ctg	atg	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240
Gly	Tyr	Gly	Leu	Met	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
65					70				75						80	

cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
				85				90						95		

acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
			100					105						110		

aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	384
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
		115					120					125				

gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
	130					135					140					

tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	ggc	480
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	
145					150				155						160	

atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac				519
Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp				
				165					170							

<210> 761

<211> 173

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; citrine F1E, w. V68L, Q69M mutations, and
posit.1 Met removed

<400> 761

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 762

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, with F64L mutation

<220>

<221> CDS
<222> (1) .. (522)

<400> 762

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5				10					15			

gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			

gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
		35					40					45				

tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55					60					

ctg	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240
Leu	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65					70				75						80	

cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85						90				95			

cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			

gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120					125				

atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130					135					140					

aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
145					150					155					160	

ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac			522
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp			
				165				170								

<210> 763
 <211> 174
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1E, with F64L mutation

<400> 763

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5				10					15		

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 764

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. F64L mutation, and posit. 1
Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 764

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96

Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu		
			20					25						30			
ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	144	
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys		
		35					40					45					
acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ctg	192	
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu		
		50				55					60						
ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240	
Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg		
65					70					75					80		
cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288	
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg		
				85					90					95			
acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336	
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val		
			100					105					110				
aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	384	
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile		
		115					120					125					
gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	432	
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn		
		130				135					140						
tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	ggc	480	
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly		
145					150					155					160		
atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac				519	
Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp					
				165					170								

<210> 765
 <211> 173
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1E, w. F64L mutation, and posit. 1
 Met removed

<400> 765

Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val
1				5					10					15	

Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu
			20					25						30	

Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35 40 45
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 766
 <211> 522
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1E, w. F64L, S65T, and Y66W mutations

<220>
 <221> CDS
 <222> (1)..(522)

<400> 766
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ctg acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	
145 150 155 160	
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
165 170	

<210> 767

<211> 174

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. F64L, S65T, and Y66W mutations

<400> 767

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 768

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. F64L, S65T, and Y66W mutations, and
posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 768

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 519
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 769

<211> 173

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. F64L, S65T, and Y66W mutations, and
 posit. 1 Met removed

<400> 769

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 770

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. F64L, S65T, Y66W, N146I, M153T,
 and V163A mutations

<220>

<221> CDS

<222> (1)..(522)

<400> 770

atg gtc agc aag ggc gag gag ctg ttc acc ggg gtc gtc ccc atc ctg	48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtc tcc ggc	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
tgc acc acc ggc aag ctg ccc gtc ccc tgg ccc acc ctc gtc acc acc	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ctg acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 522
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 771
<211> 174
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; CFP F1E, w. F64L, S65T, Y66W, N146I, M153T,
and V163A mutations

<400> 771

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly

115	120	125	
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
130	135	140	
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn			
145	150	155	160
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp			
165	170		
<210> 772			
<211> 519			
<212> DNA			
<213> Artificial			
<220>			
<223> modif. frag.; CFP F1E, w. F64L, S65T, Y66W, N146I, M153T, and V163A mutations, posit. 1 Met removed			
<220>			
<221> CDS			
<222> (1)..(519)			
<400> 772			
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc			48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val			
1 5 10 15			
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag			96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu			
20 25 30			
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc			144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys			
35 40 45			
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg			192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu			
50 55 60			
acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg			240
Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg			
65 70 75 80			
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc			288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg			
85 90 95			
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg			336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val			
100 105 110			
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc			384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile			

115

120

125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc 480
 Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 519
 Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 773
 <211> 173
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1E, w. F64L, S65T, Y66W, N146I, M153T,
 and V163A mutations, posit. 1 Met removed

<400> 773

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 774
 <211> 522
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1E, with Y66W mutation

<220>
 <221> CDS
 <222> (1)..(522)

<400> 774
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn

145 150 155 160 522

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 775
<211> 174
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; CFP F1E, with Y66W mutation

<400> 775

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 776
 <211> 519
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1E, w. Y66W mutation, and posit. 1
 Met removed

<220>
 <221> CDS
 <222> (1)..(519)

<400> 776

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
165 170	

<210> 777
 <211> 173
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1E, w. Y66W mutation, and posit. 1
 Met removed

<400> 777

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 778
 <211> 522
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1E, with Y66W, N146I mutations

 <220>
 <221> CDS
 <222> (1)..(522)

 <400> 778
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

 ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

 aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
 Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

 ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 522
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

 <210> 779
 <211> 174
 <212> PRT
 <213> Artificial

 <220>

<223> modif. frag.; CFP F1E, with Y66W, N146I mutations

<400> 779

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 780

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. Y66W, N146I mutations, and posit. 1
Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 780

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggc cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
165 170	

<210> 781

<211> 173

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. Y66W, N146I mutations, and posit. 1
Met removed

<400> 781

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 782

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, with M153T mutation

<220>

<221> CDS

<222> (1)..(522)

<400> 782

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		
			20					25					30				
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc		144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile		
		35					40					45					
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc		192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
	50					55					60						
ttc	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag		240
Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys		
65					70				75						80		
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag		288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		
				85					90					95			
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag		336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		
			100					105					110				
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc		384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly		
		115					120					125					
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac		432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		
	130					135					140						
aac	tac	aac	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag	aag	aac		480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn		
145					150					155					160		
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac				522
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp				
				165				170									

<210> 783

<211> 174

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, with M153T.mutation

<400> 783

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu		
1				5					10					15			

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		
			20					25					30				

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile		
		35					40					45					

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 784
<211> 519
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; CFP F1E, w. M153T mutation, and posit. 1
Met removed

<220>
<221> CDS
<222> (1)..(519)

<400> 784
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc	480
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
165 170	

<210> 785
 <211> 173
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1E, w. M153T mutation, and posit. 1
 Met removed

<400> 785

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 786

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, with N146I, M153T mutations

<220>

<221> CDS

<222> (1)..(522)

<400> 786

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys

65		70		75		80										
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85						90					95		
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115				120					125				
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
			130			135					140					
aac	tac	atc	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag	aag	aac	480
Asn	Tyr	Ile	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	
					150					155					160	
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac			522
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp			
				165				170								

<210> 787

<211> 174

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, with N146I, M153T mutations

<400> 787

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
			20					25					30		

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
			35				40					45			

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
	50					55					60				

Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys
65					70					75				80	

Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
				85					90					95	

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 788
<211> 519
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; CFP F1E, w. N146I, M153T mutations, and
posit.1 Met removed

<220>
<221> CDS
<222> (1)..(519)

<400> 788
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc 480
 Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 519
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 789
 <211> 173
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1E, w. N146I, M153T mutations, and
 posit.1 Met removed

<400> 789

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 790
 <211> 522
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1E, w. N146I, M153T, V163A mutations

<220>
 <221> CDS
 <222> (1)..(522)

<400> 790
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480
 Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 522
 Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 791
 <211> 174
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1E, w. N146I, M153T, V163A mutations

<400> 791

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 792
<211> 519
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; CFP F1E, w. N146I, M153T, V163A mutations, and
posit. 1 Met removed

<220>
<221> CDS
<222> (1)..(519)

<400> 792
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140
tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc 480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac
 Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

519

<210> 793
 <211> 173
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1E, w. N146I, M153T, V163A mutations, and
 posit. 1 Met removed

<400> 793

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 794
 <211> 522
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1E, w. Y66W, N146I, and M153T mutations
 <220>
 <221> CDS
 <222> (1)..(522)

<400> 794

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5				10					15			
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35				40					45				
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55				60						
ttc	ggc	tgg	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240
Phe	Gly	Trp	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65				70					75					80		
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85				90						95		
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115				120					125				
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130					135					140					
aac	tac	atc	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag	aag	aac	480
Asn	Tyr	Ile	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	
145					150					155				160		
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac			522
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp			
				165				170								

<210> 795
 <211> 174
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1E, w. Y66W, N146I, and M153T mutations
 <400> 795

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 796
 <211> 519
 <212> DNA
 <213> Artificial

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<220>
<223>  modif. frag.; CFP F1E, w. Y66W, N146I, and M153T mutations,
        and posit. 1 Met removed

<220>
<221>  CDS
<222>  (1)..(519)

<400>  796
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1                               5                               10                               15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20                               25                               30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35                               40                               45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50                               55                               60

ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                               70                               75                               80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85                               90                               95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100                              105                              110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115                              120                              125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130                              135                              140

tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc      480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145                              150                              155                              160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac      519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165                              170

<210>  797
<211>  173
<212>  PRT
<213>  Artificial

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<220>
 <223> modif. frag.; CFP F1E, w. Y66W, N146I, and M153T mutations,
 and posit. 1 Met removed

 <400> 797

 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

 Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

 Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

 <210> 798
 <211> 522
 <212> DNA
 <213> Artificial

 <220>
 <223> modif. frag.; CFP F1E, w. Y66W, N146I, M153T, and V163A mutations

 <220>
 <221> CDS

<222> (1) .. (522)

<400> 798

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 522
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 799

<211> 174

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. Y66W, N146I, M153T, and V163A mutations

<400> 799

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

1

5

10

15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 800

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. Y66W, N146I, M153T, and V163A
 mutations, and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 800

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc	480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gcc aac ttc aag atc cgc cac aac atc gag gac	519
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
165 170	
<210> 801	
<211> 173	
<212> PRT	
<213> Artificial	
<220>	
<223> modif. frag.; CFP F1E, w. Y66W, N146I, M153T, and V163A mutations, and posit. 1 Met removed	
<400> 801	
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 802
 <211> 522
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1E, with S65A mutation

<220>
 <221> CDS
 <222> (1)..(522)

<400> 802
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile

35					40					45					
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192														
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr															
50 55 60															
ttc gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240														
Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys															
65 70 75 80															
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288														
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu															
85 90 95															
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336														
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu															
100 105 110															
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384														
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly															
115 120 125															
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432														
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr															
130 135 140															
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac	480														
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn															
145 150 155 160															
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	522														
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp															
165 170															

<210> 803
 <211> 174
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1E, with S65A mutation

<400> 803

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 804

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. S65A mutation, and posit. 1
Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 804

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240

Ala	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg
65					70					75					80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
165 170	

<210> 805
 <211> 173
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1E, w. S65A mutation, and posit. 1
 Met removed

<400> 805

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 806

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. S65A, Y66W, and S72A mutations

<220>

<221> CDS

<222> (1)..(522)

<400> 806

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctg gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

	100	105	110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc				384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly				
	115	120	125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac				432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr				
	130	135	140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac				480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn				
	145	150	155	160
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac				522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp				
	165	170		

<210> 807

<211> 174

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. S65A, Y66W, and S72A mutations

<400> 807

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 808

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. S65A, Y66W, and S72A mutations,
 and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 808

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 809
<211> 173
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; CFP F1E, w. S65A, Y66W, and S72A mutations,
and posit. 1 Met removed

<400> 809

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 810

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1E, w. S65A, Y66W, S72A, N146I, M153T,
and V163A mutations

<220>

<221> CDS

<222> (1)..(522)

<400> 810

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn	
145 150 155 160	

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac
 Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

522

<210> 811
 <211> 174
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1E, w. S65A, Y66W, S72A, N146I, M153T,
 and V163A mutations

<400> 811

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 812
 <211> 519
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1E, w. S65A, Y66W, S72A, N146I, M153T,
 and V163A mutations, position 1 Met removed

<220>
 <221> CDS
 <222> (1)..(519)

<400> 812

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc	480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gcc aac ttc aag atc cgc cac aac atc gag gac	519
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
165 170	

<210> 813
 <211> 173
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1E, w. S65A, Y66W, S72A, N146I, M153T,
 and V163A mutations, position 1 Met removed

<400> 813

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 814
 <211> 522
 <212> DNA
 <213> Artificial

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<220>
<223>  modif. frag.; BFP  F1E, with Y66H mutation

<220>
<221>  CDS
<222>  (1)..(522)

<400>  814
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1          5          10          15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
          20          25          30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
          35          40          45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
          50          55          60

ttc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65          70          75          80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
          85          90          95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
          100          105          110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
          115          120          125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
          130          135          140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac      480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145          150          155          160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac      522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
          165          170

<210>  815
<211>  174
<212>  PRT
<213>  Artificial

<220>

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<223> modif. frag.; BFP F1E, with Y66H mutation

<400> 815

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 816

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1E, w. Y66H mutation, and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 816
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
 Thr Thr Gly Lys Leu Pro Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 519
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 817
 <211> 173
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; BFP F1E, w. Y66H mutation, and posit. 1 Met removed

<400> 817

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 818

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1E, with F64L, Y66H mutations

<220>

<221> CDS

<222> (1)..(522)

<400> 818

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

20										25					30					
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144				
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile					
35				40				45												
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192				
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr					
50		55				60														
ctc	ggc	cac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240				
Leu	Gly	His	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys					
65		70				75				80										
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288				
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu					
85				90				95												
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336				
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu					
100			105				110													
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384				
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly					
115			120				125													
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432				
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr					
130		135				140														
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480				
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn					
145		150				155				160										
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac			522				
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp							
165				170																

<210> 819

<211> 174

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F1E, with F64L, Y66H mutations

<400> 819

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
			20					25					30		

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
35				40				45							

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 820

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1E, w. F64L, Y66H mutations, and
posit.1 Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 820

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc 192

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
165 170	

<210> 821
 <211> 173
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; BFP F1E, w. F64L, Y66H mutations, and
 posit.1 Met removed

<400> 821

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
50 55 60	
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 822

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1E, w. F64L, Y66H, and Y145F mutations

<220>

<221> CDS

<222> (1)..(522)

<400> 822

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288

Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85					90					95		
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115				120					125				
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130					135					140					
aac	ttc	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480
Asn	Phe	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
145					150					155					160	
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac			522
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp			
				165					170							

<210> 823

<211> 174

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F1E, w. F64L, Y66H, and Y145F mutations

<400> 823

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5					10					15		

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
		35					40					45				

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55					60					

Leu	Gly	His	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65					70					75					80	

Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85					90					95		

Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105						110		

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 824

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1E, w. F64L, Y66H, and Y145F mutations,
 and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 824

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
 Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 519
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 825

<211> 173

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F1E, w. F64L, Y66H, and Y145F mutations,
 and posit. 1 Met removed

<400> 825

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 826
 <211> 522
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; BFP FlE, with Y145F mutation

<220>
 <221> CDS
 <222> (1)..(522)

<400> 826
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctg gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr

130	135	140	
aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac			480
Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn			
145	150	155	160
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac			522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp			
	165	170	
<210>	827		
<211>	174		
<212>	PRT		
<213>	Artificial		
<220>			
<223>	modif. frag.; BFP F1E, with Y145F mutation		
<400>	827		
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1	5	10	15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
	20	25	30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
	35	40	45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
	50	55	60
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys			
65	70	75	80
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
	85	90	95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
	100	105	110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
	115	120	125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
	130	135	140
Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn			
145	150	155	160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 828
<211> 519
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; BFP F1E, w. Y145F mutation, and posit. 1
Met removed

<220>
<221> CDS
<222> (1)..(519)

<400> 828
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125
gac ttc aag gag gac ggc aac atc ctg ggc cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140
ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 519

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 829
<211> 173
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; BFP F1E, w. Y145F mutation, and posit. 1
Met removed

<400> 829

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 830

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<211> 522
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; Venus F1E, with F46L mutation

<220>
<221> CDS
<222> (1)..(522)

<400> 830
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg      48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1          5          10          15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc      96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
          20          25          30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc      144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
          35          40          45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc      192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
          50          55          60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag      240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65          70          75          80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag      288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
          85          90          95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag      336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
          100          105          110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc      384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
          115          120          125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac      432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
          130          135          140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac      480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
          145          150          155          160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac      522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
          165          170

<210> 831
<211> 174
<212> PRT

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<213> Artificial

<220>

<223> modif. frag.; Venus F1E, with F46L mutation

<400> 831

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 832

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, w. F46L mutation, and posit. 1
Met removed

<220>
<221> CDS
<222> (1) .. (519)

<400> 832

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
165 170	

<210> 833
 <211> 173
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1E, w. F46L mutation, and posit. 1
 Met removed

<400> 833

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 834

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, with F46L, F64L mutations

<220>

<221> CDS

<222> (1)..(522)

<400> 834

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		
			20					25					30				
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ctg	atc		144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Leu	Ile		
		35					40					45					
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc		192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
	50					55					60						
ctg	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag		240
Leu	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys		
65					70				75					80			
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag		288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		
			85						90					95			
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag		336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		
			100					105					110				
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc		384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly		
		115					120					125					
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac		432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		
	130					135					140						
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac		480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn		
145					150				155					160			
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac				522
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp				
			165					170									

<210> 835

<211> 174

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, with F46L, F64L mutations

<400> 835

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu		
1				5					10					15			

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		
			20					25					30				

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Leu	Ile		
		35					40					45					

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 836

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, w. F46L, F64L mutations, and
posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 836

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
50 55 60	
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac	519
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
165 170	

<210> 837
 <211> 173
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1E, w. F46L, F64L mutations, and
 posit. 1 Met removed

<400> 837

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 838

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, with F46L, M153T mutations

<220>

<221> CDS

<222> (1)..(522)

<400> 838

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys

65		70		75		80										
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85						90					95		
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115				120					125				
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
			130			135					140					
aac	tac	aac	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag	aag	aac	480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	
					150					155					160	
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac			522
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp			
				165				170								

<210> 839
 <211> 174
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1E, with F46L, M153T mutations

<400> 839

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5					10					15		
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Leu	Ile	
			35				40					45				
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55					60					
Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65					70					75					80	
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85						90					95		

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 840
 <211> 519
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; Venus FlE, w. F46L, M153T mutations, and
 posit. 1 Met removed

<220>
 <221> CDS
 <222> (1)..(519)

<400> 840
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30
 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
 35 40 45
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60
 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc 480
 Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 519
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 841
 <211> 173
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1E, w. F46L, M153T mutations, and
 posit. 1 Met removed

<400> 841

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 842
 <211> 522
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1E, with F64L, M153T mutations

<220>
 <221> CDS
 <222> (1)..(522)

<400> 842
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr

130	135	140	
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac			480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn			
145	150	155	160
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac			522
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp			
	165	170	
<210>	843		
<211>	174		
<212>	PRT		
<213>	Artificial		
<220>			
<223>	modif. frag.; Venus F1E, with F64L, M153T mutations		
<400>	843		
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu			
1	5	10	15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly			
	20	25	30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile			
	35	40	45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr			
	50	55	60
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys			
65	70	75	80
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu			
	85	90	95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu			
	100	105	110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly			
	115	120	125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr			
	130	135	140
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn			
145	150	155	160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 844
<211> 519
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; Venus F1E, w.F64L, M153T mutations, and
posit. 1 Met removed

<220>
<221> CDS
<222> (1)..(519)

<400> 844
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 519

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 845
 <211> 173
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1E, w.F64L, M153T mutations, and
 posit. 1 Met removed

<400> 845

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 846

<211> 522
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1E, w. F64L, M153T, and V163A mutations

<220>
 <221> CDS
 <222> (1)..(522)

<400> 846

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5				10					15			
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35				40					45				
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55					60					
ctg	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240
Leu	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65				70					75						80	
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85						90					95		
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120					125				
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130					135					140					
aac	tac	aac	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag	aag	aac	480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	
145					150					155					160	
ggc	atc	aag	gcc	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac			522
Gly	Ile	Lys	Ala	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp			
				165				170								

<210> 847
 <211> 174

<212> PRT
<213> Artificial

<220>
<223> modif. frag.; Venus F1E, w. F64L, M153T, and V163A mutations

<400> 847

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 848
<211> 519
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; Venus F1E, w.F64L, M153T, and V163A mutations,
and posit. 1 Met removed

<220>
<221> CDS
<222> (1) .. (519)

<400> 848
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc 480
 Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 519
 Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 849

<211> 173

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, w.F64L, M153T, and V163A mutations,
 and posit. 1 Met removed

<400> 849

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 850

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, w. F46L, M153T, and V163A mutations

<220>

<221> CDS

<222> (1)..(522)

<400> 850

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

48

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile	
35 40 45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctg gtg acc acc	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggc cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn	
145 150 155 160	
ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac	522
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp	
165 170	

<210> 851

<211> 174

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, w. F46L, M153T, and V163A mutations

<400> 851

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 852
 <211> 519
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1E, w. F46L, M153T, and V163A mutations,
 and posit. 1 Met removed

<220>
 <221> CDS
 <222> (1)..(519)

<400> 852
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
 35 40 45
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60
 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140
 tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc 480
 Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160
 atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 519
 Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 853

<211> 173

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, w. F46L, M153T, and V163A mutations,
and posit. 1 Met removed

<400> 853

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 854
<211> 522
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; Venus F1E, w. F46L, F64L, M153T, and
V163A mutations

<220>
<221> CDS
<222> (1)..(522)

<400> 854
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
50						55					60						
ctg	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240	
Leu	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys		
65					70				75						80		
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288	
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu		
				85					90					95			
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336	
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu		
			100					105					110				
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384	
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly		
		115					120					125					
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432	
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		
	130					135					140						
aac	tac	aac	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag	aag	aac	480	
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn		
145					150					155					160		
ggc	atc	aag	gcc	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac			522	
Gly	Ile	Lys	Ala	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp				
				165				170									

<210> 855

<211> 174

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, w. F46L, F64L, M153T, and V163A mutations

<400> 855

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu		
1				5					10					15			

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly		
			20					25					30				

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Leu	Ile		
		35					40					45					

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr		
50						55					60						

Leu	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys		
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--	--

65																			
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu				
			85						90					95					
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu				
			100					105					110						
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly				
		115					120					125							
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr				
	130					135					140								
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn				
145					150					155					160				
Gly	Ile	Lys	Ala	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp						
				165					170										

<210> 856
 <211> 519
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1E, w. F46L, F64L, M153T, and V163A mutations, and posit. 1 Met removed

<220>
 <221> CDS
 <222> (1)..(519)

<400>	856																		
gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc				48
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val				
1			5						10					15					
gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag				96
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu				
			20				25						30						
ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ctg	atc	tgc				144
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Leu	Ile	Cys				
		35					40					45							
acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ctg				192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Leu				
	50					55					60								
ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg				240
Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg				

65

70

75

80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

gac ttc aag gag gac ggc aac atc ctg ggc cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc 480
 Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 519
 Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 857
 <211> 173
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus FlE, w. F46L, F64L, M153T, and V163A
 mutations, and posit. 1 Met removed

<400> 857

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 858

<211> 522

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus FlE, with V163A mutation

<220>

<221> CDS

<222> (1)..(522)

<400> 858

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctg gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

	100		105		110	
	gtg aag ttc gag ggc gac acc	ctg gtg aac cgc atc	gag ctg aag ggc	384		
	Val Lys Phe Glu Gly Asp Thr	Leu Val Asn Arg Ile	Glu Leu Lys Gly			
	115	120	125			
	atc gac ttc aag gag gac ggc aac	atc ctg ggg cac aag ctg gag tac	432			
	Ile Asp Phe Lys Glu Asp Gly Asn	Ile Leu Gly His Lys Leu Glu Tyr				
	130	135	140			
	aac tac aac agc cac aac gtc tat	atc atg gcc gac aag cag aag aac	480			
	Asn Tyr Asn Ser His Asn Val Tyr	Ile Met Ala Asp Lys Gln Lys Asn				
	145	150	155	160		
	ggc atc aag gcc aac ttc aag atc	cgc cac aac atc gag gac	522			
	Gly Ile Lys Ala Asn Phe Lys Ile	Arg His Asn Ile Glu Asp				
	165	170				

<210> 859

<211> 174

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus FlE, with V163A mutation

<400> 859

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1			5						10					15	

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
		20					25						30		

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
	35						40					45			

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
	50				55						60				

Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys
65				70					75					80	

Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
			85					90						95	

Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
			100					105					110		

Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
		115					120					125			

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 860
 <211> 519
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1E, w. V163A mutation, and posit. 1
 Met removed

<220>
 <221> CDS
 <222> (1)..(519)

<400> 860
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30
 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60
 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	ggc	480
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	
145					150					155					160	

<210>	861
<211>	173
<212>	PRT
<213>	Artificial

<400> 861

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
165 170

<210> 862
<211> 522
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; Venus F1E, with M153T, V163A mutations

<220>
<221> CDS
<222> (1)..(522)

<400> 862
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140
aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160
ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac 522
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp

165

170

<210> 863

<211> 174

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, with M153T, V163A mutations

<400> 863

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

<210> 864

<211> 519

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1E, w. M153T, V163A mutations, and
posit.1 Met removed

<220>

<221> CDS

<222> (1)..(519)

<400> 864

gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc	48
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
1			5						10					15		

gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag	96
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
			20					25					30			

ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	144
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
		35					40					45				

acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ttc	192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	
		50				55					60					

ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240
Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
65					70				75					80		

cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
				85					90					95		

acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
			100					105						110		

aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	384
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
		115					120					125				

gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
		130				135						140				

tac	aac	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag	aag	aac	ggc	480
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	Gly	
145					150					155					160	

atc	aag	gcc	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac				519
Ile	Lys	Ala	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp				
			165						170							

<210> 865

<211> 173

<212> PRT

<213> Artificial

<220>
 <223> modif. frag.; Venus F1E, w. M153T, V163A mutations, and
 posit.1 Met removed

 <400> 865
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140
 Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160
 Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 165 170

 <210> 866
 <211> 198
 <212> DNA
 <213> Artificial

 <220>
 <223> modif. frag.; YFP F2E, with Met added @ position 1

 <220>

<221> CDS
 <222> (1)..(198)
 <223> YFP F2E corresponds to aa residues 175-end of YFP

<400> 866
 atg ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 48
 Met Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 1 5 10 15
 ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag 96
 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
 20 25 30
 tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg 144
 Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 35 40 45
 ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg 192
 Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 50 55 60
 tac aag 198
 Tyr Lys
 65

<210> 867
 <211> 66
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; YFP F2E, with Met added @ position 1

<400> 867
 Met Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 1 5 10 15
 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
 20 25 30
 Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 35 40 45
 Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 50 55 60
 Tyr Lys
 65

<210> 868
 <211> 195
 <212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F2E, with Y203F mutation

<220>

<221> CDS

<222> (1)..(195)

<400> 868

ggc	agc	gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	48
Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	
1				5					10					15		

gac	ggc	ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	ttc	cag	tcc	96
Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Phe	Gln	Ser	
			20					25					30			

gcc	ctg	agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	144
Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	
			35				40					45				

gag	ttc	gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	192
Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	
	50					55					60					

aag																195
Lys																
65																

<210> 869

<211> 65

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F2E, with Y203F mutation

<400> 869

Gly	Ser	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly
1				5					10					15	

Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Phe	Gln	Ser
			20					25					30		

Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu
			35				40					45			

Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr
	50					55					60				

Lys															
65															

<210> 870
 <211> 198
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; YFP F2E, w. Y203F mutation, Met added @ posit. 1

<220>
 <221> CDS
 <222> (1)..(198)

<400> 870
 atg ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 48
 Met Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 1 5 10 15
 ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc ttc cag 96
 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln
 20 25 30
 tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg 144
 Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 35 40 45
 ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg 192
 Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 50 55 60
 tac aag 198
 Tyr Lys
 65

<210> 871
 <211> 66
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; YFP F2E, w. Y203F mutation, Met added @ posit. 1

<400> 871
 Met Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 1 5 10 15
 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln
 20 25 30
 Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 35 40 45
 Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 50 55 60

Tyr Lys
65

<210> 872
<211> 195
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; YFP F2E, with Y203H mutation

<220>
<221> CDS
<222> (1)..(195)

<400> 872
ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 48
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
1 5 10 15
gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc cac cag tcc 96
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser
20 25 30
gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 144
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
35 40 45
gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 192
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
50 55 60
aag 195
Lys
65

<210> 873
<211> 65
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; YFP F2E, with Y203H mutation

<400> 873

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
1 5 10 15
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser
20 25 30
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
35 40 45

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
50 55 60

Lys
65

<210> 874
<211> 198
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; YFP F2E, w. Y203H mutation, Met added @ posit. 1

<220>
<221> CDS
<222> (1)..(198)

<400> 874
atg ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 48
Met Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
1 5 10 15
ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc cac cag 96
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln
20 25 30
tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg 144
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
35 40 45
ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg 192
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
50 55 60
tac aag 198
Tyr Lys
65

<210> 875
<211> 66
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; YFP F2E, w. Y203H mutation, Met added @ posit. 1

<400> 875

Met Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
1 5 10 15
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln
20 25 30

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 35 40 45

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 50 55 60

Tyr Lys
 65

<210> 876
 <211> 195
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; Venus F2E, with S175G mutation

<220>
 <221> CDS
 <222> (1)..(195)

<400> 876
 ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 48
 Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 1 5 10 15

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc 96
 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
 20 25 30

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 144
 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 35 40 45

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 192
 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 50 55 60

aag 195
 Lys
 65

<210> 877
 <211> 65
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F2E, with S175G mutation

<400> 877

Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 1 5 10 15

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
20 25 30

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
35 40 45

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
50 55 60

Lys
65

<210> 878
<211> 198
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; Venus F2E, w. S175G mutation , Met added @ posit. 1
<220>
<221> CDS
<222> (1)..(198)

<400> 878
atg ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 48
Met Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
1 5 10 15
ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag 96
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
20 25 30
tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg 144
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
35 40 45
ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg 192
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
50 55 60
tac aag 198
Tyr Lys
65

<210> 879
<211> 66
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; Venus F2E, w. S175G mutation , Met added @ posit. 1

<400> 879

Met Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 1 5 10 15

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
 20 25 30

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 35 40 45

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 50 55 60

Tyr Lys
 65

<210> 880
 <211> 195
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; Venus F2E, w. S175G, Y203T mutations

<220>
 <221> CDS
 <222> (1)..(195)

<400> 880
 ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 48
 Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 1 5 10 15

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc 96
 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
 20 25 30

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 144
 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 35 40 45

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 192
 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 50 55 60

aag 195
 Lys
 65

<210> 881
 <211> 65
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F2E, w. S175G, Y203T mutations
 <400> 881

Gly	Gly	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly
1				5					10					15	

Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser
			20					25					30		

Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu
		35					40					45			

Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr
50						55					60				

Lys
 65

<210> 882
 <211> 198
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; Venus F2E, w. S175G, Y203T mutations, and
 Met added @ position 1

<220>
 <221> CDS
 <222> (1)..(198)

<400> 882

atg	ggc	ggc	gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	48
Met	Gly	Gly	Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	
1				5					10					15		

ggc	gac	ggc	ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	acc	cag	96
Gly	Asp	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	
			20					25					30			

tcc	gcc	ctg	agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	144
Ser	Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	
		35					40					45				

ctg	gag	ttc	gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	192
Leu	Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	
	50					55					60					

tac	aag	198
Tyr	Lys	
65		

<210> 883
 <211> 66
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F2E, w. S175G, Y203T mutations, and
 Met added @ position 1

<400> 883

Met Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 1 5 10 15

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
 20 25 30

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 35 40 45

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 50 55 60

Tyr Lys
 65

<210> 884
 <211> 195
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; Venus F2E, w. S175G, Y203F mutations

<220>
 <221> CDS
 <222> (1)..(195)

<400> 884

ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 48
 Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 1 5 10 15

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc ttc cag tcc 96
 Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln Ser
 20 25 30

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 144
 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 35 40 45

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 192
 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 50 55 60

aag
Lys
65

195

<210> 885
<211> 65
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; Venus F2E, w. S175G, Y203F mutations

<400> 885

Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
5 10 15

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln Ser
20 25 30

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
35 40 45

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
50 55 60

Lys
65

<210> 886
<211> 198
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; Venus F2E, w. S175G, Y203F mutations, and
Met added @ position 1

<220>
<221> CDS
<222> (1)..(198)

<400> 886

atg ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc
Met Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
1 5 10 15

48

ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc ttc cag
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln
20 25 30

96

tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg	144
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu	
35 40 45	
ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg	192
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu	
50 55 60	
tac aag	198
Tyr Lys	
65	

<210> 887
 <211> 66
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F2E, w. S175G, Y203F mutations, and
 Met added @ position 1

<400> 887

Met Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 1 5 10 15

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln
 20 25 30

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 35 40 45

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 50 55 60

Tyr Lys
 65

<210> 888
 <211> 570
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; YFP F1F, with position 1 Met removed

<220>
 <221> CDS
 <222> (1)..(570)
 <223> YFP F1F corresponds to aa residues 1-191 of YFP

<400> 888

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60
 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140
 tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160
 atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg 528
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175
 cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 889

<211> 190

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1F, with position 1 Met removed

<400> 889

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 890
<211> 573
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; YFP F1F, with K79R mutation

<220>
<221> CDS
<222> (1)..(573)

<400> 890
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile

35					40					45						
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
50						55					60					
ttc	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	cgc	240
Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Arg	
65					70					75					80	
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85					90					95		
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120					125				
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130					135					140					
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
145					150					155					160	
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
				165				170						175		
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac		573
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp		
			180					185					190			

<210> 891

<211> 191

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1F, with K79R mutation

<400> 891

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
			20					25					30		

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
		35					40					45			

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 892

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1F, w. K79R mutation, and posit. 1
Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 892

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctg gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg cgc cgg	240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
165 170 175	
cag ctg gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
180 185 190	

<210> 893

<211> 190

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1F, w. K79R mutation, and posit. 1
Met removed

<400> 893

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Arg Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 894
 <211> 573
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; YFP F1F, with Y66F mutation

<220>
 <221> CDS
 <222> (1)..(573)

<400> 894
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

20										25					30					
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144				
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile					
35				40				45												
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192				
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr					
50		55				60														
ttc	ggc	ttc	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240				
Phe	Gly	Phe	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys					
65		70				75				80										
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288				
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu					
85				90				95												
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336				
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu					
100			105				110													
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384				
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly					
115			120				125													
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432				
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr					
130		135				140														
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480				
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn					
145		150				155				160										
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528				
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser					
165				170				175												
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac		573				
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp						
180			185				190													

<210> 895

<211> 191

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1F, with Y66F mutation

<400> 895

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
20			25				30								

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 896

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1F, w. Y66F mutation, and posit. 1
 Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 896

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctg gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
ggc ttc ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
165 170 175	
cag ctg gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
180 185 190	

<210> 897

<211> 190

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1F, w. Y66F mutation, and posit. 1
Met removed

<400> 897

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Phe Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 898

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F1F, with Q69K mutation

<220>

<221> CDS

<222> (1)..(573)

<400> 898

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

20										25					30					
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144				
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile					
35			40			45														
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192				
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr					
50		55		60																
ttc	ggc	tac	ggc	ctg	aag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240				
Phe	Gly	Tyr	Gly	Leu	Lys	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys					
65		70		75		80														
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288				
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu					
85			90			95														
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336				
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu					
100			105			110														
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384				
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly					
115		120		125																
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432				
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr					
130		135		140																
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480				
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn					
145		150		155		160														
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528				
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser					
165			170			175														
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac		573				
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp						
180			185			190														

<210> 899

<211> 191

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1F, with Q69K mutation

<400> 899

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
			20					25					30		

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 900
<211> 570
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; YFP F1F, w. Q69K mutation, and posit. 1
Met removed

<220>
<221> CDS
<222> (1)..(570)

<400> 900
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctg gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
165 170 175	
cag ctg gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
180 185 190	

<210> 901

<211> 190

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F1F, w. Q69K mutation, and posit. 1
Met removed

<400> 901

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 902
 <211> 573
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; citrine F1F, w. V68L, Q69M mutations

<220>
 <221> CDS
 <222> (1)..(573)

<400> 902
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

20										25					30					
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144				
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile					
35			40			45														
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192				
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr					
50		55		60																
ttc	ggc	tac	ggc	ctg	atg	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240				
Phe	Gly	Tyr	Gly	Leu	Met	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys					
65	70			75			80													
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288				
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu					
85			90			95														
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336				
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu					
100			105			110														
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384				
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly					
115			120			125														
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432				
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr					
130	135			140																
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480				
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn					
145	150			155			160													
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528				
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser					
165			170			175														
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac		573				
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp						
180			185			190														

<210> 903

<211> 191

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; citrine F1F, w. V68L, Q69M mutations

<400> 903

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
			20					25					30		

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 904
 <211> 570
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; citrine F1F, w. V68L, Q69M mutations, and
 posit. 1 Met removed

<220>
 <221> CDS
 <222> (1)..(570)

<400> 904
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
ggc tac ggc ctg atg tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
165 170 175	
cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
180 185 190	

<210> 905

<211> 190

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; citrine F1F, w. V68L, Q69M mutations, and
posit. 1 Met removed

<400> 905

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 906
 <211> 573
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1F, with F64L mutation

<220>
 <221> CDS
 <222> (1)..(573)

<400> 906
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

20										25					30					
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144				
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile					
35				40				45												
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192				
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr					
50		55				60														
ctg	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240				
Leu	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys					
65		70				75				80										
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288				
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu					
85				90				95												
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336				
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu					
100			105				110													
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384				
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly					
115			120				125													
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432				
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr					
130		135				140														
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480				
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn					
145		150				155				160										
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528				
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser					
165				170				175												
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac		573				
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp						
180			185				190													

<210> 907

<211> 191

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, with F64L mutation

<400> 907

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
20			25				30								

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 908

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. F64L mutation, posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 908

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu

20

25

30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctg gtg acc acc ctg	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
50 55 60	
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
165 170 175	
cag ctg gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
180 185 190	

<210> 909

<211> 190

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. F64L mutation, posit. 1 Met removed

<400> 909

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 910
 <211> 573
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1F, w. F64L, S65T, and Y66W mutations

<220>
 <221> CDS
 <222> (1)..(573)

<400> 910
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

20										25					30					
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144				
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile					
35						40			45											
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192				
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr					
50						55				60										
ctg	acc	tgg	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240				
Leu	Thr	Trp	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys					
65				70				75				80								
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288				
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu					
			85						90			95								
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336				
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu					
			100			105						110								
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384				
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly					
115						120						125								
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432				
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr					
130						135				140										
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480				
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn					
145				150				155				160								
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528				
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser					
			165						170			175								
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac		573				
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp						
			180			185						190								

<210> 911

<211> 191

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. F64L, S65T, and Y66W mutations

<400> 911

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
			20					25					30		

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 912
 <211> 570
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1F, w. F64L, S65T, and Y66W mutations,
 and posit. 1 Met removed

<220>
 <221> CDS
 <222> (1)..(570)

<400> 912
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

48

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu 20 25 30	96
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys 35 40 45	144
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctg gtg acc acc ctg Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu 50 55 60	192
acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg 65 70 75 80	240
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg 85 90 95	288
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val 100 105 110	336
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile 115 120 125	384
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn 130 135 140	432
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly 145 150 155 160	480
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val 165 170 175	528
cag ctg gcc gac cac tac cag cag aac acc ccc atc ggc gac Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp 180 185 190	570

<210> 913

<211> 190

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. F64L, S65T, and Y66W mutations,
and posit. 1 Met removed

<400> 913

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val 1 5 10 15
--

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 914

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. F64L, S65T, Y66W, N146I, M153T,
 and V163A mutations

<220>

<221> CDS

<222> (1) .. (573)

<400> 914
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 915
<211> 191
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; CFP F1F, w. F64L, S65T, Y66W, N146I, M153T,
and V163A mutations

<400> 915

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 916

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. F64L, S65T, Y66W, N146I, M153T,
and V163A mutations, and position 1 Met removed

<220>

<221> CDS
 <222> (1)..(570)

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<400> 916
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1          5          10          15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
          20          25          30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
          35          40          45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
          50          55          60

acc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65          70          75          80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
          85          90          95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
          100          105          110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
          115          120          125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
          130          135          140

tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc      480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145          150          155          160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg      528
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
          165          170          175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac      570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
          180          185          190

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<210> 917
 <211> 190
 <212> PRT
 <213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. F64L, S65T, Y66W, N146I, M153T,
and V163A mutations, and position 1 Met removed

<400> 917

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Thr Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 918

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, with Y66W mutation

<220>
 <221> CDS
 <222> (1)..(573)

<400> 918

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5				10					15			

gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			

gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35				40					45				

tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55				60						

ttc	ggc	tgg	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240
Phe	Gly	Trp	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65				70					75					80		

cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85					90						95		

cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			

gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120					125				

atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130					135					140					

aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
145					150					155					160	

ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
				165				170						175		

gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac		573
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp		
			180				185						190			

<210> 919
 <211> 191
 <212> PRT
 <213> Artificial

<220>

<223> modif. frag.; CFP F1F, with Y66W mutation

<400> 919

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 920

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. Y66W mutation, and posit. 1 Met removed

<220>
 <221> CDS
 <222> (1)..(570)

<400> 920

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
165 170 175	
cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
180 185 190	

<210> 921
 <211> 190
 <212> PRT
 <213> Artificial

<220>
<223> modif. frag.; CFP F1F, w. Y66W mutation, and posit. 1 Met removed

<400> 921

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 922

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. Y66W, N146I mutations

<220>
<221> CDS
<222> (1)..(573)

<400> 922
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac atc agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 923

<211> 191

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. Y66W, N146I mutations

<400> 923

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 924
<211> 570
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; CFP F1F, w. Y66W, N146I mutations, and
posit. 1 Met removed

<220>
<221> CDS

<222> (1)..(570)

<400> 924

gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc	48
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
1			5					10					15			

gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag	96
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
		20					25						30			

ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	144
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
		35					40					45				

acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ttc	192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	
	50					55					60					

ggc	tgg	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240
Gly	Trp	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
65				70				75						80		

cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
				85				90					95			

acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
			100					105					110			

aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	384
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
		115					120					125				

gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
	130					135					140					

tac	atc	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	ggc	480
Tyr	Ile	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly	
145					150					155					160	

atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	gtg	528
Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	
			165						170					175		

cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac			570
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp			
			180					185					190			

<210> 925

<211> 190

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. Y66W, N146I mutations, and
posit. 1 Met removed

<400> 925

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 926

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, with M153T mutation

<220>

<221> CDS
<222> (1) .. (573)

<400> 926
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480
 Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160
 ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 573
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190
 <210> 927
 <211> 191
 <212> PRT
 <213> Artificial
 <220>
 <223> modif. frag.; CFP F1F, with M153T mutation

<400> 927

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 928

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. M153T mutation, and posit. 1 Met removed

<220>
 <221> CDS
 <222> (1)..(570)

 <400> 928
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

 gac ttc aag gag gac ggc aac atc ctg ggc cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

 tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc 480
 Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

 atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg 528
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

 cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

 <210> 929
 <211> 190
 <212> PRT
 <213> Artificial

 <220>

<223> modif. frag.; CFP F1F, w. M153T mutation, and posit. 1 Met removed

<400> 929

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 930

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, with M153T mutation

<220>
 <221> CDS
 <222> (1)..(573)

<400> 930

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggc cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn	
145 150 155 160	
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
180 185 190	

<210> 931
 <211> 191
 <212> PRT
 <213> Artificial

<220>

<223> modif. frag.; CFP F1F, with M153T mutation

<400> 931

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 932

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. N146I, M153T mutations, and

posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 932

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc	480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
165 170 175	
cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
180 185 190	

<210> 933

<211> 190

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. N146I, M153T mutations, and
posit. 1 Met removed

<400> 933

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 934

<211> 573

<212> DNA

<213> Artificial

<220>
 <223> modif. frag.; CFP F1F, w. N146I, M153T, and V163A mutations

 <220>
 <221> CDS
 <222> (1)..(573)

 <400> 934
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctg gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

 ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

 aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480
 Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

 ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
 Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

 gtg cag ctg gcc gac cac tac cag cag aac acc ccc atc ggc gac 573
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

 <210> 935
 <211> 191
 <212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. N146I, M153T, and V163A mutations

<400> 935

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 936

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. N146I, M153T, and V163A mutations,
and posit. 1 Met removed

<220>

<221> CDS

<222> (1) .. (570)

<400> 936

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctg gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc	480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
165 170 175	
cag ctg gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
180 185 190	

<210> 937

<211> 190

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. N146I, M153T, and V163A mutations,

and posit. 1 Met removed

<400> 937

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 938

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. Y66W, N146I, and M153T mutations

<220>
 <221> CDS
 <222> (1)..(573)

<400> 938
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480
 Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160
 ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 573
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 939
 <211> 191
 <212> PRT
 <213> Artificial

<220>
<223> modif. frag.; CFP F1F, w. Y66W, N146I, and M153T mutations

<400> 939

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 940

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. Y66W, N146I, and M153T mutations,

and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 940

gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc	48
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
1				5					10					15		

gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag	96
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
			20					25					30			

ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	144
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
		35					40					45				

acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ttc	192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	
	50					55					60					

ggc	tgg	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240
Gly	Trp	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
65				70					75						80	

cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
				85					90					95		

acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
			100					105					110			

aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	384
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
		115					120					125				

gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
	130					135					140					

tac	atc	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag	aag	aac	ggc	480
Tyr	Ile	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	Gly	
145					150					155					160	

atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	gtg	528
Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val	
				165				170						175		

cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac			570
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp			
			180					185					190			

<210> 941

<211> 190

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. Y66W, N146I, and M153T mutations,
and posit. 1 Met removed

<400> 941

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 942

<211> 573

<212> DNA

<213> Artificial

<220>
 <223> modif. frag.; CFP F1F, w. Y66W, N146I, M153T, and V163A mutations

<220>
 <221> CDS
 <222> (1)..(573)

<400> 942

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	
35 40 45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ttc ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn	
145 150 155 160	
ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
180 185 190	

<210> 943
 <211> 191
 <212> PRT
 <213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. Y66W, N146I, M153T, and V163A mutations

<400> 943

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 944

<211> 570
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1F, w. Y66W, N146I, M153T, and V163A mutations, and posit. 1 Met removed

<220>
 <221> CDS
 <222> (1)..(570)

<400> 944

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
ggc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc	480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
165 170 175	
cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	

180 185 190

<210> 945
 <211> 190
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1F, w. Y66W, N146I, M153T, and V163A mutations, and posit. 1 Met removed

<400> 945

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 946
 <211> 573
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1F, with S65A mutation

<220>
 <221> CDS
 <222> (1)..(573)

<400> 946

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5				10					15			
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35				40					45				
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55				60						
ttc	gcc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240
Phe	Ala	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65				70					75					80		
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85					90						95		
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115				120					125				
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130					135					140					
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
145					150					155					160	
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
				165				170						175		
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac		573

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 947
<211> 191
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; CFP F1F, with S65A mutation

<400> 947

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 948
 <211> 570
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1F, w. S65A mutation, and posit. 1
 Met removed

<220>
 <221> CDS
 <222> (1)..(570)

<400> 948

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
gcc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
165 170 175	

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

570

<210> 949
 <211> 190
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1F, w. S65A mutation, and posit. 1
 Met removed

<400> 949

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Ala Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 950
<211> 573
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; CFP F1F, w. S65A, Y66W, and S72A mutations

<220>
<221> CDS
<222> (1)..(573)

<400> 950
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctg gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60
ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140
aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser

165 170 175
 gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 573
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

 <210> 951
 <211> 191
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; CFP F1F, w. S65A, Y66W, and S72A mutations

 <400> 951

 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

 Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 952

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. S65A, Y66W, and S72A mutations,
and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 952

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg 528
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 953
 <211> 190
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1F, w. S65A, Y66W, and S72A mutations,
 and posit. 1 Met removed

<400> 953

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 954

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; CFP F1F, w. S65A, Y66W, S72A, N146I, M153T,
and V163A mutations

<220>

<221> CDS

<222> (1)..(573)

<400> 954

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc gcc tgg ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
 Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 573
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 955
 <211> 191
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; CFP F1F, w. S65A, Y66W, S72A, N146I, M153T,
 and V163A mutations

<400> 955

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn

130	135	140	
tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc			480
Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly			
145	150	155	160
atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg			528
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val			
	165	170	175
cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac			570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp			
	180	185	190
<210> 957			
<211> 190			
<212> PRT			
<213> Artificial			
<220>			
<223> modif. frag.; CFP F1F, w. S65A, Y66W, S72A, N146I, M153T, and V163A mutations, and posit. 1 Met removed			
<400> 957			
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val			
1	5	10	15
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu			
	20	25	30
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys			
	35	40	45
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe			
	50	55	60
Ala Trp Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg			
65	70	75	80
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg			
	85	90	95
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val			
	100	105	110
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile			
	115	120	125
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn			
	130	135	140

Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 958
 <211> 573
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; BFP F1F, with Y66H mutation

<220>
 <221> CDS
 <222> (1)..(573)

<400> 958
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctg gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 ttc ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432

Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
130						135					140					
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
145					150					155					160	
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
				165					170					175		
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac		573
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp		
			180					185					190			

<210> 959
 <211> 191
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; BFP F1F, with Y66H mutation

<400> 959

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5					10					15		
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35				40					45				
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55					60					
Phe	Gly	His	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65					70					75				80		
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85						90					95		
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
			115				120					125				
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
130						135					140					

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 960

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1F, w. Y66H mutation, and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 960

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg 528
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 961
 <211> 190
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; BFP F1F, w. Y66H mutation, and posit. 1 Met removed

<400> 961

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 962

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1F, w. F64L, Y66H mutations

<220>

<221> CDS

<222> (1)..(573)

<400> 962

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctg gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432

Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr		
130						135					140						
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480	
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn		
145					150					155					160		
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528	
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser		
				165					170					175			
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac		573	
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp			
			180					185					190				

<210> 963
 <211> 191
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; BFP F1F, w. F64L, Y66H mutations

<400> 963

Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu
1				5					10					15	

Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly
			20					25					30		

Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
		35					40					45			

Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
	50					55					60				

Leu	Gly	His	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys
65					70					75					80

Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
			85						90					95	

Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu
			100					105					110		

Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly
		115					120					125			

Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr
130						135					140				

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 964

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1F, w. F64L, Y66H mutations, and
posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 964
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30
 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60
 ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140
 tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160
 atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg 528
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175
 cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190
 <210> 965
 <211> 190
 <212> PRT
 <213> Artificial
 <220>
 <223> modif. frag.; BFP F1F, w. F64L, Y66H mutations, and
 posit. 1 Met removed

<400> 965

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 966

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1F, w. F64L, Y66H, and Y145F mutations

<220>

<221> CDS

<222> (1) .. (573)

<400> 966

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5					10					15		

gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			

gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
		35					40					45				

tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55					60					

ctg	ggc	cac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240
Leu	Gly	His	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65					70				75						80	

cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85					90					95		

cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			

gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120					125				

atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130					135					140					

aac	ttc	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480
Asn	Phe	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
145					150				155						160	

ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
				165				170						175		

gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac		573
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp		
			180				185						190			

<210> 967

<211> 191

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F1F, w. F64L, Y66H, and Y145F mutations

<400> 967

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 968

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1F, w. F64L, Y66H, and Y145F mutations,
and posit. 1 Met removed

<220>
 <221> CDS
 <222> (1)..(570)

<400> 968

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
50 55 60	
ggc cac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc	480
Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
165 170 175	
cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
180 185 190	

<210> 969
 <211> 190
 <212> PRT
 <213> Artificial

<220>

<223> modif. frag.; BFP F1F, w. F64L, Y66H, and Y145F mutations,
and posit. 1 Met removed

<400> 969

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Gly His Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 970

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1F, with Y145F mutation

<220>

<221> CDS

<222> (1)..(573)

<400> 970

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1			5					10					15			

gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			

gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
		35					40					45				

tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55					60					

ttc	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240
Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65					70				75						80	

cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85					90						95		

cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			

gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120					125				

atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130					135					140					

aac	ttc	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480
Asn	Phe	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
145					150				155						160	

ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
			165					170						175		

gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac		573
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp		
			180					185					190			

<210> 971

<211> 191

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; BFP F1F, with Y145F mutation

<400> 971

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 972

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; BFP F1F, w. Y145F mutation, and posit. 1 Met removed

<220>
 <221> CDS
 <222> (1)..(570)

 <400> 972
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

 gac ttc aag gag gac ggc aac atc ctg ggc cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

 ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
 Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

 atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg 528
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

 cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

 <210> 973
 <211> 190
 <212> PRT
 <213> Artificial

 <220>

<223> modif. frag.; BFP F1F, w. Y145F mutation, and posit. 1 Met removed

<400> 973

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 974

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. F46L, F64L, M153T, V163A mutations

<220>
 <221> CDS
 <222> (1)..(573)

<400> 974

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg	48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu	
1 5 10 15	
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc	96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly	
20 25 30	
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc	144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile	
35 40 45	
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc	192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	
50 55 60	
ctg ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag	240
Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	
65 70 75 80	
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag	288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	
85 90 95	
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag	336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	
100 105 110	
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc	384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	
115 120 125	
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac	432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	
130 135 140	
aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac	480
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn	
145 150 155 160	
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc	528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	
165 170 175	
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
180 185 190	

<210> 975
 <211> 191
 <212> PRT
 <213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. F46L, F64L, M153T, V163A mutations

<400> 975

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 976

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. F46L, F64L, M153T, V163A mutations,
and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 976

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
50 55 60	
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc	480
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg	528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	
165 170 175	
cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
180 185 190	

<210> 977

<211> 190
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1F, w. F46L, F64L, M153T, V163A mutations,
 and posit. 1 Met removed

<400> 977

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 978
 <211> 573

<212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1F, with V163A mutation

<220>
 <221> CDS
 <222> (1)..(573)

<400> 978

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5					10					15		
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
		35					40					45				
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55					60					
ttc	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240
Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65					70					75					80	
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85						90					95		
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120					125				
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130					135					140					
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
145					150					155					160	
ggc	atc	aag	gcc	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528
Gly	Ile	Lys	Ala	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
			165					170						175		
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac		573
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp		
			180					185					190			

<210> 979
 <211> 191
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1F, with V163A mutation

<400> 979

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 980
 <211> 570

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<212> DNA
<213> Artificial

<220>
<223> modif. frag.; Venus F1F, w. V163A mutation, posit. 1 Met removed

<220>
<221> CDS
<222> (1)..(570)

<400> 980
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1                               5                               10                               15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20                               25                               30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35                               40                               45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50                               55                               60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65                               70                               75                               80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85                               90                               95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100                              105                              110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115                              120                              125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130                              135                              140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc      480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                              150                              155                              160

atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg      528
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165                              170                              175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac      570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180                              185                              190

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<210> 981
 <211> 190
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1F, w. V163A mutation, posit. 1 Met removed
 <400> 981

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 982
 <211> 573

<212> DNA
<213> Artificial

<220>
<223> modif. frag.; Venus F1F, w. M153T, V163A mutations

<220>
<221> CDS
<222> (1)..(573)

<400> 982

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5					10					15		
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
		35					40					45				
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55					60					
ttc	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240
Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65					70				75						80	
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85					90					95		
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120					125				
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130					135					140					
aac	tac	aac	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag	aag	aac	480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	
145					150					155					160	
ggc	atc	aag	gcc	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	agc	528
Gly	Ile	Lys	Ala	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	
				165				170						175		
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac		573
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp		
			180					185					190			

<210> 983
 <211> 191<212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1F, w. M153T, V163A mutations

<400> 983

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 984

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. M153T, V163A mutations, and
posit. 1 Met removed

<220>
 <221> CDS
 <222> (1)..(570)

 <400> 984
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctg gtg acc acc ttc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

 gac ttc aag gag gac ggc aac atc ctg ggc cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

 tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc 480
 Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

 atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg 528
 Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

 cag ctg gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

 <210> 985
 <211> 190
 <212> PRT
 <213> Artificial

 <220>

<223> modif. frag.; Venus F1F, w. M153T, V163A mutations, and
posit. 1 Met removed

<400> 985

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 986

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, with S175G mutation

<220>
 <221> CDS
 <222> (1)..(573)

<400> 986

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5					10					15		
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	
			35				40					45				
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55					60					
ttc	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240
Phe	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65					70				75					80		
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
				85					90					95		
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120					125				
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130					135					140					
aac	tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	aag	aac	480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	
145					150					155					160	
ggc	atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	ggc	528
Gly	Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Gly	
				165				170						175		
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac		573
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp		
			180					185					190			

<210> 987
 <211> 191
 <212> PRT
 <213> Artificial

<220>

<223> modif. frag.; Venus F1F, with S175G mutation

<400> 987

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 988

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. S175G mutation, posit. 1 Met removed

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<220>
<221> CDS
<222> (1)..(570)

<400> 988
gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc      48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1          5          10          15

gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20          25          30

ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc      144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35          40          45

acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc      192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50          55          60

ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg      240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65          70          75          80

cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc      288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85          90          95

acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg      336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100          105          110

aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc      384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115          120          125

gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130          135          140

tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc      480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145          150          155          160

atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg      528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
165          170          175

cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac      570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180          185          190

<210> 989
<211> 190
<212> PRT
<213> Artificial

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<220>

<223> modif. frag.; Venus F1F, w. S175G mutation, posit. 1 Met removed

<400> 989

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 990
 <211> 573
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1F, w. M153T, S175G mutations

<220>
 <221> CDS
 <222> (1)..(573)

<400> 990
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15
gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60
ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80
cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140
aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160
ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc ggc 528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly
165 170 175
gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 573
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 991

<211> 191

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. M153T, S175G mutations

<400> 991

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 992

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. M153T, S175G mutations, and
posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 992

gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc	48
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
1			5						10					15		

gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag	96
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
		20					25						30			

ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	144
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
		35					40						45			

acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ttc	192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	
	50					55					60					

ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cgg	240
Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Arg	
65				70				75						80		

cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
				85				90						95		

acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
			100					105					110			

aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	384
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
		115					120					125				

gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
	130					135						140				

tac	aac	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag	aag	aac	ggc	480
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	Gly	
145					150					155					160	

atc	aag	gtg	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	ggc	gtg	528
Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Gly	Val	
			165						170					175		

cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac			570
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp			
			180					185					190			

<210> 993

<211> 190

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. M153T, S175G mutations, and
posit. 1 Met removed

<400> 993

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 994

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. V163A, S175G mutations

<220>

<221> CDS
 <222> (1)..(573)

 <400> 994
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

 ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

 aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

 ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc ggc 528
 Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly
 165 170 175

 gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 573
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

 <210> 995
 <211> 191
 <212> PRT
 <213> Artificial

 <220>
 <223> modif. frag.; Venus F1F, w. V163A, S175G mutations

<400> 995

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 996

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. V163A, S175G mutations, and
posit.1 Met removed

<220>
 <221> CDS
 <222> (1)..(570)

 <400> 996
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg 240
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

 tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc 480
 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

 atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg 528
 Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
 165 170 175

 cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 570
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

 <210> 997
 <211> 190
 <212> PRT
 <213> Artificial

 <220>

<223> modif. frag.; Venus F1F, w. V163A, S175G mutations, and
posit.1 Met removed

<400> 997

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 998

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. M153T, V163A, and S175G mutations

<220>
 <221> CDS
 <222> (1)..(573)

<400> 998
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 cgg cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 aac tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480
 Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160
 ggc atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc ggc 528
 Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly
 165 170 175
 gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 573
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 999
 <211> 191
 <212> PRT
 <213> Artificial

<220>
<223> modif. frag.; Venus F1F, w. M153T, V163A, and S175G mutations

<400> 999

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 1000

<211> 570

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. M153T, V163A, and S175G mutations,
and posit. 1 Met removed

<220>

<221> CDS

<222> (1)..(570)

<400> 1000

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys	
35 40 45	
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ttc	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe	
50 55 60	
 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
 tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc	480
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
 atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg	528
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val	
165 170 175	
 cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp	
180 185 190	

<210> 1001

<211> 190

<212> PRT
 <213> Artificial
 <220>
 <223> modif. frag.; Venus F1F, w. M153T, V163A, and S175G mutations,
 and posit. 1 Met removed

<400> 1001

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 1002

<211> 573

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. F46L, F64L, M153T, V163A, and S175G mutations

<220>

<221> CDS

<222> (1)..(573)

<400> 1002

atg	gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	48
Met	Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	
1				5				10					15			
gtc	gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	96
Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	
			20					25					30			
gag	ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ctg	atc	144
Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Leu	Ile	
			35				40					45				
tgc	acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	192
Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	
	50					55					60					
ctg	ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	240
Leu	Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	
65				70					75						80	
cgg	cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	288
Arg	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	
			85					90					95			
cgc	acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	336
Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	
			100					105					110			
gtg	aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	384
Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	
		115					120					125				
atc	gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	432
Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	
	130					135					140					
aac	tac	aac	agc	cac	aac	gtc	tat	atc	acc	gcc	gac	aag	cag	aag	aac	480
Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Thr	Ala	Asp	Lys	Gln	Lys	Asn	
145				150					155						160	
ggc	atc	aag	gcc	aac	ttc	aag	atc	cgc	cac	aac	atc	gag	gac	ggc	ggc	528
Gly	Ile	Lys	Ala	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Gly	
			165					170						175		
gtg	cag	ctc	gcc	gac	cac	tac	cag	cag	aac	acc	ccc	atc	ggc	gac		573
Val	Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp		
			180				185						190			

<210> 1003
 <211> 191
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1F, w. F46L, F64L, M153T, V163A, and S175G mutations

<400> 1003

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 1004
 <211> 570
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; Venus F1F, w. F46L, F64L, M153T, V163A, and
 S175G mutations, and posit. 1 Met removed

<220>
 <221> CDS
 <222> (1)..(570)

<400> 1004

gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc	48
Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val	
1 5 10 15	
gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag	96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu	
20 25 30	
ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ctg atc tgc	144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys	
35 40 45	
acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg	192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu	
50 55 60	
ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cgg	240
Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg	
65 70 75 80	
cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc	288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg	
85 90 95	
acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg	336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val	
100 105 110	
aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc	384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile	
115 120 125	
gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac	432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn	
130 135 140	
tac aac agc cac aac gtc tat atc acc gcc gac aag cag aag aac ggc	480
Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly	
145 150 155 160	
atc aag gcc aac ttc aag atc cgc cac aac atc gag gac ggc ggc gtg	528
Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val	
165 170 175	
cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac	570

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
180 185 190

<210> 1005

<211> 190

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; Venus F1F, w. F46L, F64L, M153T, V163A, and
S175G mutations, and posit. 1 Met removed

<400> 1005

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Arg
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Gly Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 180 185 190

<210> 1006

<211> 147

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F2F, with Met added @ position 1

<220>

<221> CDS

<222> (1)..(147)

<223> YFP F2F corresponds to aa residues 192-end of YFP

<400> 1006

atg ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc 48
 Met Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
 1 5 10 15

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 96
 Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 20 25 30

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 144
 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 35 40 45

aag 147
 Lys

<210> 1007

<211> 49

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F2F, with Met added @ position 1

<400> 1007

Met Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
 1 5 10 15

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 20 25 30

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 35 40 45

Lys

<210> 1008
 <211> 144
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; YFP F2F, with Y203F mutation

<220>
 <221> CDS
 <222> (1)..(144)

<400> 1008
 ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc ttc cag tcc gcc 48
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln Ser Ala
 1 5 10 15
 ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag 96
 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 20 25 30
 ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag 144
 Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 35 40 45

<210> 1009
 <211> 48
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; YFP F2F, with Y203F mutation

<400> 1009

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln Ser Ala
 1 5 10 15
 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 20 25 30
 Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 35 40 45

<210> 1010
 <211> 147
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; YFP F2F, w. Y203F mutation, Met added @ posit. 1

<220>
 <221> CDS

<400> 1010

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 96
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
20 25 30

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 144
 Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 35 40 45

aag 147
 Lys

<210> 1011
 <211> 49
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; YFP F2F, w. Y203F mutation, Met added @ posit. 1

<400> 1011

Met Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Phe Gln Ser
 1 5 10 15

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 20 25 30

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 35 40 45

Lys

<210> 1012
 <211> 144
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; YFP F2F, with Y203H mutation

<220>
 <221> CDS
 <222> (1)..(144)

<400> 1012

ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc cac cag tcc gcc 48
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser Ala
 1 5 10 15

ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag 96
 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 20 25 30

ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag 144
 Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 35 40 45

<210> 1013
 <211> 48
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; YFP F2F, with Y203H mutation

<400> 1013

Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	His	Gln	Ser	Ala
1				5					10					15	

Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu
			20					25					30		

Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	Lys
			35				40					45			

<210> 1014
 <211> 147
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; YFP F2F, w. Y203H mutation, Met added @ posit. 1

<220>
 <221> CDS
 <222> (1)..(147)

<400> 1014

atg	ggc	ccc	gtg	ctg	ctg	ccc	gac	aac	cac	tac	ctg	agc	cac	cag	tcc	48
Met	Gly	Pro	Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	His	Gln	Ser	
1				5					10					15		

gcc	ctg	agc	aaa	gac	ccc	aac	gag	aag	cgc	gat	cac	atg	gtc	ctg	ctg	96
Ala	Leu	Ser	Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	
			20					25					30			

gag	ttc	gtg	acc	gcc	gcc	ggg	atc	act	ctc	ggc	atg	gac	gag	ctg	tac	144
Glu	Phe	Val	Thr	Ala	Ala	Gly	Ile	Thr	Leu	Gly	Met	Asp	Glu	Leu	Tyr	
			35				40					45				

aag	147
Lys	

<210> 1015
 <211> 49
 <212> PRT
 <213> Artificial

<220>

<223> modif. frag.; YFP F2F, w. Y203H mutation, Met added @ posit. 1

<400> 1015

Met Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser His Gln Ser
1 5 10 15

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
20 25 30

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
35 40 45

Lys

<210> 1016

<211> 144

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F2F, with Y203T mutation

<220>

<221> CDS

<222> (1)..(144)

<400> 1016

ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc 48
Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
1 5 10 15

ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag 96
Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
20 25 30

ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag 144
Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
35 40 45

<210> 1017

<211> 48

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F2F, with Y203T mutation

<400> 1017

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
1 5 10 15

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
20 25 30

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
35 40 45

<210> 1018

<211> 147

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; YFP F2F, w. Y203T mutation, Met added @ posit. 1

<220>

<221> CDS

<222> (1)..(147)

<400> 1018

atg ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc 48
Met Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
1 5 10 15

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 96
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
20 25 30

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 144
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
35 40 45

aag 147
Lys

<210> 1019

<211> 49

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; YFP F2F, w. Y203T mutation, Met added @ posit. 1

<400> 1019

Met Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
1 5 10 15

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
20 25 30

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
35 40 45

Lys

<210> 1020
<211> 114
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; RFP F1A, with position 1 Met removed

<220>
<221> CDS
<222> (1)..(114)
<223> RFP F1A corresponds to aa residues 1-39 of mRFP

<400> 1020
gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc 48
Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg
1 5 10 15

atg gag ggc tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc 96
Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
20 25 30

gag ggc cgc ccc tac gag 114
Glu Gly Arg Pro Tyr Glu
35

<210> 1021
<211> 38
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; RFP F1A, with position 1 Met removed

<400> 1021

Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg
1 5 10 15

Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
20 25 30

Glu Gly Arg Pro Tyr Glu
35

<210> 1022
<211> 561
<212> DNA
<213> Artificial

<220>

<223> modif. frag.; RFP F2A, with Met added @ position 1

<220>

<221> CDS

<222> (1) ... (561)

<223> RFP F2A corresponds to aa residues 40-end of mRFP

<400> 1022

atg ggc acc cag acc gcc aag ctg aag gtg acc aag ggc ggc ccc ctg	48
Met Gly Thr Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly Pro Leu	
1 5 10 15	
ccc ttc gcc tgg gac atc ctg tcc cct cag ttc cag tac ggc tcc aag	96
Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln Tyr Gly Ser Lys	
20 25 30	
gcc tac gtg aag cac ccc gcc gac atc ccc gac tac ttg aag ctg tcc	144
Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr Leu Lys Leu Ser	
35 40 45	
ttc ccc gag ggc ttc aag tgg gag cgc gtg atg aac ttc gag gac ggc	192
Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn Phe Glu Asp Gly	
50 55 60	
ggc gtg gtg acc gtg acc cag gac tcc tcc ctg cag gac ggc gag ttc	240
Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly Glu Phe	
65 70 75 80	
atc tac aag gtg aag ctg cgc ggc acc aac ttc ccc tcc gac ggc ccc	288
Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp Gly Pro	
85 90 95	
gta atg cag aag aag acc atg ggc tgg gag gcc tcc acc gag cgg atg	336
Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu Arg Met	
100 105 110	
tac ccc gag gac ggc gcc ctg aag ggc gag atc aag atg agg ctg aag	384
Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg Leu Lys	
115 120 125	
ctg aag gac ggc ggc cac tac gac gcc gag gtc aag acc acc tac atg	432
Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met	
130 135 140	
gcc aag aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac atc aag	480
Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys	
145 150 155 160	
ctg gac atc acc tcc cac aac gag gac tac acc atc gtg gaa cag tac	528
Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr	
165 170 175	
gag cgc gcc gag ggc cgc cac tcc acc ggc gcc	561
Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala	
180 185	

<210> 1023

<211> 187

<212> PRT
<213> Artificial

<220>
<223> modif. frag.; RFP F2A, with Met added @ position 1

<400> 1023

Met Gly Thr Gln Thr Ala Lys Leu Lys Val Thr Lys Gly Gly Pro Leu
1 5 10 15

Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe Gln Tyr Gly Ser Lys
20 25 30

Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp Tyr Leu Lys Leu Ser
35 40 45

Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met Asn Phe Glu Asp Gly
50 55 60

Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly Glu Phe
65 70 75 80

Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp Gly Pro
85 90 95

Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu Arg Met
100 105 110

Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg Leu Lys
115 120 125

Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met
130 135 140

Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys
145 150 155 160

Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr
165 170 175

Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala
180 185

<210> 1024
<211> 300
<212> DNA
<213> Artificial

<220>
 <223> modif. frag.; RFP F1B, with position 1 Met removed

<220>
 <221> CDS
 <222> (1)..(300)
 <223> RFP F1B corresponds to aa residues 1-100 of mRFP

<400> 1024
 gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc 48
 Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg
 1 5 10 15
 atg gag ggc tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc 96
 Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
 20 25 30
 gag ggc cgc ccc tac gag ggc acc cag acc gcc aag ctg aag gtg acc 144
 Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr
 35 40 45
 aag ggc ggc ccc ctg ccc ttc gcc tgg gac atc ctg tcc cct cag ttc 192
 Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe
 50 55 60
 cag tac ggc tcc aag gcc tac gtg aag cac ccc gcc gac atc ccc gac 240
 Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp
 65 70 75 80
 tac ttg aag ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg atg 288
 Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met
 85 90 95
 aac ttc gag gac 300
 Asn Phe Glu Asp
 100

<210> 1025
 <211> 100
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; RFP F1B, with position 1 Met removed

<400> 1025
 Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg
 1 5 10 15
 Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
 20 25 30
 Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr
 35 40 45

Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe
 50 55 60

Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp
 65 70 75 80

Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met
 85 90 95

Asn Phe Glu Asp
 100

<210> 1026

<211> 375

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; RFP F2B, with Met added @ position 1

<220>

<221> CDS

<222> (1)..(375)

<223> RFP F2B corresponds to aa residues 102-225(end) of mRFP

<400> 1026

atg ggc ggc gtg gtg acc gtg acc cag gac tcc tcc ctg cag gac ggc 48
 Met Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly
 1 5 10 15

gag ttc atc tac aag gtg aag ctg cgc ggc acc aac ttc ccc tcc gac 96
 Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp
 20 25 30

ggc ccc gta atg cag aag aag acc atg ggc tgg gag gcc tcc acc gag 144
 Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu
 35 40 45

cgg atg tac ccc gag gac ggc gcc ctg aag ggc gag atc aag atg agg 192
 Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg
 50 55 60

ctg aag ctg aag gac ggc ggc cac tac gac gcc gag gtc aag acc acc 240
 Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr
 65 70 75 80

tac atg gcc aag aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac 288
 Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp
 85 90 95

atc aag ctg gac atc acc tcc cac aac gag gac tac acc atc gtg gaa 336
 Ile Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu
 100 105 110

cag tac gag cgc gcc gag ggc cgc cac tcc acc ggc gcc
 Gln Tyr Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala
 115 120 125

<210> 1027

<211> 125

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; RFP F2B, with Met added @ position 1

<400> 1027

Met Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu Gln Asp Gly
 1 5 10 15

Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro Ser Asp
 20 25 30

Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser Thr Glu
 35 40 45

Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg
 50 55 60

Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr
 65 70 75 80

Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp
 85 90 95

Ile Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu
 100 105 110

Gln Tyr Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala
 115 120 125

<210> 1028

<211> 342

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; RFP F1C, with position 1 Met removed

<220>

<221> CDS

<222> (1)..(342)

<223> RFP F1C corresponds to aa residues 1-115 of mRFP

<400> 1028
gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc 48
Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg
1 5 10 15
atg gag ggc tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc 96
Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
20 25 30
gag ggc cgc ccc tac gag ggc acc cag acc gcc aag ctg aag gtg acc 144
Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr
35 40 45
aag ggc ggc ccc ctg ccc ttc gcc tgg gac atc ctg tcc cct cag ttc 192
Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe
50 55 60
cag tac ggc tcc aag gcc tac gtg aag cac ccc gcc gac atc ccc gac 240
Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp
65 70 75 80
tac ttg aag ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg atg 288
Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met
85 90 95
aac ttc gag gac ggc ggc gtg gtg acc gtg acc cag gac tcc tcc ctg 336
Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu
100 105 110
cag gac 342
Gln Asp

<210> 1029
<211> 114
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; RFP F1C, with position 1 Met removed

<400> 1029
Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg
1 5 10 15
Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
20 25 30
Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr
35 40 45
Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe
50 55 60

Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp
65 70 75 80

Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met
85 90 95

Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu
100 105 110

Gln Asp

<210> 1030

<211> 333

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; RFP F2C, with Met added @ position 1

<220>

<221> CDS

<222> (1)..(333)

<223> RFP F2C corresponds to aa residues 116-225(end) of mRFP

<400> 1030

atg ggc gag ttc atc tac aag gtg aag ctg cgc ggc acc aac ttc ccc 48
Met Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro
1 5 10 15

tcc gac ggc ccc gta atg cag aag aag acc atg ggc tgg gag gcc tcc 96
Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser
20 25 30

acc gag cgg atg tac ccc gag gac ggc gcc ctg aag ggc gag atc aag 144
Thr Glu Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys
35 40 45

atg agg ctg aag ctg aag gac ggc ggc cac tac gac gcc gag gtc aag 192
Met Arg Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys
50 55 60

acc acc tac atg gcc aag aag ccc gtg cag ctg ccc ggc gcc tac aag 240
Thr Thr Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys
65 70 75 80

acc gac atc aag ctg gac atc acc tcc cac aac gag gac tac acc atc 288
Thr Asp Ile Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile
85 90 95

gtg gaa cag tac gag cgc gcc gag ggc cgc cac tcc acc ggc gcc 333
Val Glu Gln Tyr Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala
100 105 110

<210> 1031

<211> 111

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; RFP F2C, with Met added @ position 1

<400> 1031

Met Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe Pro
1 5 10 15

Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala Ser
20 25 30

Thr Glu Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile Lys
35 40 45

Met Arg Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val Lys
50 55 60

Thr Thr Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys
65 70 75 80

Thr Asp Ile Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile
85 90 95

Val Glu Gln Tyr Glu Arg Ala Glu Gly Arg His Ser Thr Gly Ala
100 105 110

<210> 1032

<211> 456

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; RFP F1D, with position 1 Met removed

<220>

<221> CDS

<222> (1)..(456)

<223> RFP F1D corresponds to aa residues 1-153 of mRFP

<400> 1032

gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc 48
Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg
1 5 10 15

atg gag ggc tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc 96
Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
20 25 30

gag ggc cgc ccc tac gag ggc acc cag acc gcc aag ctg aag gtg acc 144
Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr
35 40 45

aag ggc ggc ccc ctg ccc ttc gcc tgg gac atc ctg tcc cct cag ttc 192
Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe

50	55	60	
cag tac ggc tcc aag gcc tac gtg aag cac ccc gcc gac atc ccc gac			240
Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp			
65	70	75	80
tac ttg aag ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg atg			288
Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met			
	85	90	95
aac ttc gag gac ggc ggc gtg gtg acc gtg acc cag gac tcc tcc ctg			336
Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu			
	100	105	110
cag gac ggc gag ttc atc tac aag gtg aag ctg cgc ggc acc aac ttc			384
Gln Asp Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe			
	115	120	125
ccc tcc gac ggc ccc gta atg cag aag aag acc atg ggc tgg gag gcc			432
Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala			
	130	135	140
tcc acc gag cgg atg tac ccc gag			456
Ser Thr Glu Arg Met Tyr Pro Glu			
145	150		

<210> 1033

<211> 152

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; RFP F1D, with position 1 Met removed

<400> 1033

Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg
1 5 10 15

Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
20 25 30

Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr
35 40 45

Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe
50 55 60

Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp
65 70 75 80

Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met
85 90 95

Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu
100 105 110

Gln Asp Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe
115 120 125

Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala
130 135 140

Ser Thr Glu Arg Met Tyr Pro Glu
145 150

<210> 1034
<211> 219
<212> DNA
<213> Artificial

<220>
<223> modif. frag.; RFP F2D, with Met added @ position 1

<220>
<221> CDS
<222> (1)..(219)
<223> RFP F2D corresponds to aa residues 154-225(end) of mRFP

<400> 1034
atg gac ggc gcc ctg aag ggc gag atc aag atg agg ctg aag ctg aag 48
Met Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg Leu Lys Leu Lys
1 5 10 15
gac ggc ggc cac tac gac gcc gag gtc aag acc acc tac atg gcc aag 96
Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met Ala Lys
20 25 30
aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac atc aag ctg gac 144
Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys Leu Asp
35 40 45
atc acc tcc cac aac gag gac tac acc atc gtg gaa cag tac gag cgc 192
Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr Glu Arg
50 55 60
gcc gag ggc cgc cac tcc acc ggc gcc 219
Ala Glu Gly Arg His Ser Thr Gly Ala
65 70

<210> 1035
<211> 73
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; RFP F2D, with Met added @ position 1

<400> 1035

Met Asp Gly Ala Leu Lys Gly Glu Ile Lys Met Arg Leu Lys Leu Lys
 1 5 10 15

Asp Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met Ala Lys
 20 25 30

Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys Leu Asp
 35 40 45

Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr Glu Arg
 50 55 60

Ala Glu Gly Arg His Ser Thr Gly Ala
 65 70

<210> 1036

<211> 504

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; RFP F1E, with position 1 Met removed

<220>

<221> CDS

<222> (1)..(504)

<223> RFP F1E corresponds to aa residues 1-169 of mRFP

<400> 1036

gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc 48
 Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg
 1 5 10 15

atg gag ggc tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc 96
 Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
 20 25 30

gag ggc cgc ccc tac gag ggc acc cag acc gcc aag ctg aag gtg acc 144
 Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr
 35 40 45

aag ggc ggc ccc ctg ccc ttc gcc tgg gac atc ctg tcc cct cag ttc 192
 Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe
 50 55 60

cag tac ggc tcc aag gcc tac gtg aag cac ccc gcc gac atc ccc gac 240
 Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp
 65 70 75 80

tac ttg aag ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg atg 288
 Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met
 85 90 95

aac ttc gag gac ggc ggc gtg gtg acc gtg acc cag gac tcc tcc ctg	336
Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu	
100 105 110	

cag gac ggc gag ttc atc tac aag gtg aag ctg cgc ggc acc aac ttc	384
Gln Asp Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe	
115 120 125	

ccc tcc gac ggc ccc gta atg cag aag aag acc atg ggc tgg gag gcc	432
Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala	
130 135 140	

tcc acc gag cgg atg tac ccc gag gac ggc gcc ctg aag ggc gag atc	480
Ser Thr Glu Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile	
145 150 155 160	

aag atg agg ctg aag ctg aag gac	504
Lys Met Arg Leu Lys Leu Lys Asp	
165	

<210> 1037
 <211> 168
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; RFP FlE, with position 1 Met removed
 <400> 1037

Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg
1 5 10 15

Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
20 25 30

Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr
35 40 45

Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe
50 55 60

Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp
65 70 75 80

Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met
85 90 95

Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu
100 105 110

Gln Asp Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe
 115 120 125

Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala
 130 135 140

Ser Thr Glu Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile
 145 150 155 160

Lys Met Arg Leu Lys Leu Lys Asp
 165

<210> 1038

<211> 171

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; RFP F2E, with Met added @ position 1

<220>

<221> CDS

<222> (1)..(171)

<223> RFP F2E corresponds to aa residues 170-225(end) of mRFP

<400> 1038

atg ggc ggc cac tac gac gcc gag gtc aag acc acc tac atg gcc aag 48
 Met Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met Ala Lys
 1 5 10 15

aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac atc aag ctg gac 96
 Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys Leu Asp
 20 25 30

atc acc tcc cac aac gag gac tac acc atc gtg gaa cag tac gag cgc 144
 Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr Glu Arg
 35 40 45

gcc gag ggc cgc cac tcc acc ggc gcc 171
 Ala Glu Gly Arg His Ser Thr Gly Ala
 50 55

<210> 1039

<211> 57

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; RFP F2E, with Met added @ position 1

<400> 1039

Met Gly Gly His Tyr Asp Ala Glu Val Lys Thr Thr Tyr Met Ala Lys


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1              5              10              15
Lys  Pro  Val  Gln  Leu  Pro  Gly  Ala  Tyr  Lys  Thr  Asp  Ile  Lys  Leu  Asp
      20              25              30
Ile  Thr  Ser  His  Asn  Glu  Asp  Tyr  Thr  Ile  Val  Glu  Gln  Tyr  Glu  Arg
      35              40              45
Ala  Glu  Gly  Arg  His  Ser  Thr  Gly  Ala
      50              55

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<400>	1040																
gcc tcc tcc gag gac gtc atc aag gag ttc atg cgc ttc aag gtg cgc																	48
Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg																	
1				5				10						15			
atg gag ggc tcc gtg aac ggc cac gag ttc gag atc gag ggc gag ggc																	96
Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly																	
			20					25					30				
gag ggc cgc ccc tac gag ggc acc cag acc gcc aag ctg aag gtg acc																	144
Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr																	
		35					40					45					
aag ggc ggc ccc ctg ccc ttc gcc tgg gac atc ctg tcc cct cag ttc																	192
Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe																	
	50					55				60							
cag tac ggc tcc aag gcc tac gtg aag cac ccc gcc gac atc ccc gac																	240
Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp																	
65					70				75						80		
tac ttg aag ctg tcc ttc ccc gag ggc ttc aag tgg gag cgc gtg atg																	288
Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met																	
			85					90					95				
aac ttc gag gac ggc ggc gtg gtg acc gtg acc cag gac tcc tcc ctg																	336
Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu																	
			100					105					110				
cag gac ggc gag ttc atc tac aag gtg aag ctg cgc ggc acc aac ttc																	384
Gln Asp Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe																	

115	120	125	
ccc tcc gac ggc ccc gta atg cag aag aag acc atg ggc tgg gag gcc			432
Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala			
130	135	140	
tcc acc gag cgg atg tac ccc gag gac ggc gcc ctg aag ggc gag atc			480
Ser Thr Glu Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile			
145	150	155	160
aag atg agg ctg aag ctg aag gac ggc ggc cac tac gac gcc gag gtc			528
Lys Met Arg Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val			
165	170	175	
aag acc acc tac atg gcc aag			549
Lys Thr Thr Tyr Met Ala Lys			
180			

<210> 1041
 <211> 183
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; RFP F1F, with position 1 Met removed

<400> 1041

Ala Ser Ser Glu Asp Val Ile Lys Glu Phe Met Arg Phe Lys Val Arg
1 5 10 15

Met Glu Gly Ser Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu Gly
20 25 30

Glu Gly Arg Pro Tyr Glu Gly Thr Gln Thr Ala Lys Leu Lys Val Thr
35 40 45

Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln Phe
50 55 60

Gln Tyr Gly Ser Lys Ala Tyr Val Lys His Pro Ala Asp Ile Pro Asp
65 70 75 80

Tyr Leu Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met
85 90 95

Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu
100 105 110

Gln Asp Gly Glu Phe Ile Tyr Lys Val Lys Leu Arg Gly Thr Asn Phe
115 120 125

Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu Ala
 130 135 140

Ser Thr Glu Arg Met Tyr Pro Glu Asp Gly Ala Leu Lys Gly Glu Ile
 145 150 155 160

Lys Met Arg Leu Lys Leu Lys Asp Gly Gly His Tyr Asp Ala Glu Val
 165 170 175

Lys Thr Thr Tyr Met Ala Lys
 180

<210> 1042

<211> 126

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; RFP F2F, with Met added @ position 1

<220>

<221> CDS

<222> (1)..(126)

<223> RFP F2F corresponds to aa residues 185-225(end) of mRFP

<400> 1042

atg aag ccc gtg cag ctg ccc ggc gcc tac aag acc gac atc aag ctg	48
Met Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys Leu	
1 5 10 15	

gac atc acc tcc cac aac gag gac tac acc atc gtg gaa cag tac gag	96
Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr Glu	
20 25 30	

cgc gcc gag ggc cgc cac tcc acc ggc gcc	126
Arg Ala Glu Gly Arg His Ser Thr Gly Ala	
35 40	

<210> 1043

<211> 42

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; RFP F2F, with Met added @ position 1

<400> 1043

Met Lys Pro Val Gln Leu Pro Gly Ala Tyr Lys Thr Asp Ile Lys Leu
1 5 10 15

Asp Ile Thr Ser His Asn Glu Asp Tyr Thr Ile Val Glu Gln Tyr Glu

20

25

30

Arg Ala Glu Gly Arg His Ser Thr Gly Ala
 35 40

<210> 1044
 <211> 105
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; KFP F1A, with position 1 Met removed

<220>
 <221> CDS
 <222> (1)..(105)
 <223> KFP F1A corresponds to aa residues 1-36 of KFP1

<400> 1044
 gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag ggc 48
 Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly
 1 5 10 15
 acc gtg aac ggc cac tgc ttc aag tgc atc ggc aag ggc gag ggc aac 96
 Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn
 20 25 30
 ccc ttc gag 105
 Pro Phe Glu
 35

<210> 1045
 <211> 35
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; KFP F1A, with position 1 Met removed

<400> 1045
 Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly
 1 5 10 15
 Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn
 20 25 30
 Pro Phe Glu
 35

<210> 1046
 <211> 591
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; KFP F2A, with Met added @ position 1

<220>
 <221> CDS
 <222> (1)..(591)
 <223> KFP F2A corresponds to aa residues 37-end of KFP1

<400> 1046

atg ggc acc cag gag atg aag atc gag gtg atc gag ggc ggc ccc ctg	48
Met Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly Pro Leu	
1 5 10 15	
ccc ttc gcc ttc cac atc ctg tcc acc tcc tgc atg tac ggc tcc aag	96
Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly Ser Lys	
20 25 30	
acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc aag cag tcc	144
Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys Gln Ser	
35 40 45	
ttc ccc gag ggc ttc acc tgg gag cgc acc acc acc tac gag gac ggc	192
Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu Asp Gly	
50 55 60	
ggc ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc gac tgc ctg	240
Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp Cys Leu	
65 70 75 80	
gtg tac aag gtg aag atc ctg ggt aac aac ttc ccc gcc gac ggc ccc	288
Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp Gly Pro	
85 90 95	
gtg atg cag aac aag gtc ggc cgc tgg gag ccc gga acc gag atc gtg	336
Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu Ile Val	
100 105 110	
tac gag gtg gac ggc gtg ctg cgc ggc cag tcc ctg atg gcc ctg aag	384
Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala Leu Lys	
115 120 125	
tgc ccc ggc ggc cgg cac ctg acc tgc cac ctg cac acc acc tac cgc	432
Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr Thr Tyr Arg	
130 135 140	
tcc aag aag ccc gcc tcc gcc ctg aag atg ccc ggc ttc cac ttc gag	480
Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly Phe His Phe Glu	
145 150 155 160	
gac cac cgc atc gag atc atg gag gag gtg gag aag ggc aag tgc tac	528
Asp His Arg Ile Glu Ile Met Glu Glu Val Glu Lys Gly Lys Cys Tyr	
165 170 175	
aag cag tac gag gcc gcc gtg ggc cgc tac tgc gac gcc gcc ccc tcc	576
Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp Ala Ala Pro Ser	
180 185 190	
aag ctg ggc cac aac	591
Lys Leu Gly His Asn	

195

<210> 1047

<211> 197

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; KFP F2A, with Met added @ position 1

<400> 1047

Met Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly Pro Leu
1 5 10 15

Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly Ser Lys
20 25 30

Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys Gln Ser
35 40 45

Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu Asp Gly
50 55 60

Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp Cys Leu
65 70 75 80

Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp Gly Pro
85 90 95

Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu Ile Val
100 105 110

Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala Leu Lys
115 120 125

Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr Thr Tyr Arg
130 135 140

Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly Phe His Phe Glu
145 150 155 160

Asp His Arg Ile Glu Ile Met Glu Glu Val Glu Lys Gly Lys Cys Tyr
165 170 175

Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp Ala Ala Pro Ser
180 185 190

Lys Leu Gly His Asn
195

<210> 1048

<211> 291

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; KFP F1B, with position 1 Met removed

<220>

<221> CDS

<222> (1)..(291)

<223> KFP F1B corresponds to aa residues 1-98 of KFP1

<400> 1048

gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag ggc	48
Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly	
1 5 10 15	

acc gtg aac ggc cac tgc ttc aag tgc atc ggc aag ggc gag ggc aac	96
Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn	
20 25 30	

ccc ttc gag ggc acc cag gag atg aag atc gag gtg atc gag ggc ggc	144
Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly	
35 40 45	

ccc ctg ccc ttc gcc ttc cac atc ctg tcc acc tcc tgc atg tac ggc	192
Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly	
50 55 60	

tcc aag acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc aag	240
Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys	
65 70 75 80	

cag tcc ttc ccc gag ggc ttc acc tgg gag cgc acc acc acc tac gag	288
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu	
85 90 95	

gac	291
Asp	

<210> 1049

<211> 97

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; KFP F1B, with position 1 Met removed

<400> 1049

Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly

1

5

10

15

Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn
 20 25 30

Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly
 35 40 45

Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly
 50 55 60

Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys
 65 70 75 80

Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu
 85 90 95

Asp

<210> 1050

<211> 405

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; KFP F2B, with Met added @ position 1

<220>

<221> CDS

<222> (1)..(405)

<223> KFP F2B corresponds to aa residues 99-end of KFP1

<400> 1050

atg ggc ggc ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc gac 48
 Met Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp
 1 5 10 15

tgc ctg gtg tac aag gtg aag atc ctg ggt aac aac ttc ccc gcc gac 96
 Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp
 20 25 30

ggc ccc gtg atg cag aac aag gtc ggc cgc tgg gag ccc gga acc gag 144
 Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu
 35 40 45

atc gtg tac gag gtg gac ggc gtg ctg cgc ggc cag tcc ctg atg gcc 192
 Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala
 50 55 60

ctg aag tgc ccc ggc ggc cgg cac ctg acc tgc cac ctg cac acc acc 240
 Leu Lys Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr Thr
 65 70 75 80

tac cgc tcc aag aag ccc gcc tcc gcc ctg aag atg ccc ggc ttc cac	288
Tyr Arg Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly Phe His	
85 90 95	

ttc gag gac cac cgc atc gag atc atg gag gag gtg gag aag ggc aag	336
Phe Glu Asp His Arg Ile Glu Ile Met Glu Glu Val Glu Lys Gly Lys	
100 105 110	

tgc tac aag cag tac gag gcc gcc gtg ggc cgc tac tgc gac gcc gcc	384
Cys Tyr Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp Ala Ala	
115 120 125	

ccc tcc aag ctg ggc cac aac	405
Pro Ser Lys Leu Gly His Asn	
130 135	

<210> 1051
 <211> 135
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; KFP F2B, with Met added @ position 1

<400> 1051

Met Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp
1 5 10 15

Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp
20 25 30

Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu
35 40 45

Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala
50 55 60

Leu Lys Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr Thr
65 70 75 80

Tyr Arg Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly Phe His
85 90 95

Phe Glu Asp His Arg Ile Glu Ile Met Glu Glu Val Glu Lys Gly Lys
100 105 110

Cys Tyr Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp Ala Ala
115 120 125

Pro Ser Lys Leu Gly His Asn
130 135

<210> 1052

<211> 456

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; KFP F1C, with position 1 Met removed

<220>

<221> CDS

<222> (1)..(456)

<223> KFP F1C corresponds to aa residues 1-153 of KFP1

<400> 1052

gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag ggc	48
Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly	
1 5 10 15	
acc gtg aac ggc cac tgc ttc aag tgc atc ggc aag ggc gag ggc aac	96
Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn	
20 25 30	
ccc ttc gag ggc acc cag gag atg aag atc gag gtg atc gag ggc ggc	144
Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly	
35 40 45	
ccc ctg ccc ttc gcc ttc cac atc ctg tcc acc tcc tgc atg tac ggc	192
Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly	
50 55 60	
tcc aag acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc aag	240
Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys	
65 70 75 80	
cag tcc ttc ccc gag ggc ttc acc tgg gag cgc acc acc acc tac gag	288
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu	
85 90 95	
gac ggc ggc ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc gac	336
Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp	
100 105 110	
tgc ctg gtg tac aag gtg aag atc ctg ggt aac aac ttc ccc gcc gac	384
Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp	
115 120 125	
ggc ccc gtg atg cag aac aag gtc ggc cgc tgg gag ccc gga acc gag	432
Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu	
130 135 140	
atc gtg tac gag gtg gac ggc gtg	456
Ile Val Tyr Glu Val Asp Gly Val	
145 150	

<210> 1053
 <211> 152
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; KFP F1C, with position 1 Met removed
 <400> 1053

Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly
 1 5 10 15

Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn
 20 25 30

Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly
 35 40 45

Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly
 50 55 60

Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys
 65 70 75 80

Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu
 85 90 95

Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp
 100 105 110

Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp
 115 120 125

Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu
 130 135 140

Ile Val Tyr Glu Val Asp Gly Val
 145 150

<210> 1054
 <211> 240
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; KFP F2C, with Met added @ position 1
 <220>

<221> CDS
 <222> (1)..(240)
 <223> KFP F2C corresponds to aa residues 154-end of KFP1

<400> 1054
 atg ctg cgc ggc cag tcc ctg atg gcc ctg aag tgc ccc ggc ggc cgg 48
 Met Leu Arg Gly Gln Ser Leu Met Ala Leu Lys Cys Pro Gly Gly Arg
 1 5 10 15
 cac ctg acc tgc cac ctg cac acc acc tac cgc tcc aag aag ccc gcc 96
 His Leu Thr Cys His Leu His Thr Thr Tyr Arg Ser Lys Lys Pro Ala
 20 25 30
 tcc gcc ctg aag atg ccc ggc ttc cac ttc gag gac cac cgc atc gag 144
 Ser Ala Leu Lys Met Pro Gly Phe His Phe Glu Asp His Arg Ile Glu
 35 40 45
 atc atg gag gag gtg gag aag ggc aag tgc tac aag cag tac gag gcc 192
 Ile Met Glu Glu Val Glu Lys Gly Lys Cys Tyr Lys Gln Tyr Glu Ala
 50 55 60
 gcc gtg ggc cgc tac tgc gac gcc gcc ccc tcc aag ctg ggc cac aac 240
 Ala Val Gly Arg Tyr Cys Asp Ala Ala Pro Ser Lys Leu Gly His Asn
 65 70 75 80

<210> 1055
 <211> 80
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; KFP F2C, with Met added @ position 1

<400> 1055
 Met Leu Arg Gly Gln Ser Leu Met Ala Leu Lys Cys Pro Gly Gly Arg
 1 5 10 15
 His Leu Thr Cys His Leu His Thr Thr Tyr Arg Ser Lys Lys Pro Ala
 20 25 30
 Ser Ala Leu Lys Met Pro Gly Phe His Phe Glu Asp His Arg Ile Glu
 35 40 45
 Ile Met Glu Glu Val Glu Lys Gly Lys Cys Tyr Lys Gln Tyr Glu Ala
 50 55 60
 Ala Val Gly Arg Tyr Cys Asp Ala Ala Pro Ser Lys Leu Gly His Asn
 65 70 75 80

<210> 1056
 <211> 333
 <212> DNA

<213> Artificial

<220>

<223> modif. frag.; KFP F1D, with position 1 Met removed

<220>

<221> CDS

<222> (1)..(333)

<223> KFP F1D corresponds to aa residues 1-112 of KFP1

<400> 1056

gcc	tcc	ctg	ctg	acc	gag	acc	atg	ccc	ttc	aag	acc	acc	atc	gag	ggc	48
Ala	Ser	Leu	Leu	Thr	Glu	Thr	Met	Pro	Phe	Lys	Thr	Thr	Ile	Glu	Gly	
1				5					10					15		

acc	gtg	aac	ggc	cac	tgc	ttc	aag	tgc	atc	ggc	aag	ggc	gag	ggc	aac	96
Thr	Val	Asn	Gly	His	Cys	Phe	Lys	Cys	Ile	Gly	Lys	Gly	Glu	Gly	Asn	
			20					25					30			

ccc	ttc	gag	ggc	acc	cag	gag	atg	aag	atc	gag	gtg	atc	gag	ggc	ggc	144
Pro	Phe	Glu	Gly	Thr	Gln	Glu	Met	Lys	Ile	Glu	Val	Ile	Glu	Gly	Gly	
		35					40					45				

ccc	ctg	ccc	ttc	gcc	ttc	cac	atc	ctg	tcc	acc	tcc	tgc	atg	tac	ggc	192
Pro	Leu	Pro	Phe	Ala	Phe	His	Ile	Leu	Ser	Thr	Ser	Cys	Met	Tyr	Gly	
	50					55					60					

tcc	aag	acc	ttc	atc	aag	tac	gtg	tcc	ggc	atc	ccc	gac	tac	ttc	aag	240
Ser	Lys	Thr	Phe	Ile	Lys	Tyr	Val	Ser	Gly	Ile	Pro	Asp	Tyr	Phe	Lys	
65					70					75					80	

cag	tcc	ttc	ccc	gag	ggc	ttc	acc	tgg	gag	cgc	acc	acc	acc	tac	gag	288
Gln	Ser	Phe	Pro	Glu	Gly	Phe	Thr	Trp	Glu	Arg	Thr	Thr	Thr	Tyr	Glu	
				85					90					95		

gac	ggc	ggc	ttc	ctg	acc	gcc	cac	cag	gac	acc	tcc	ctg	gac	ggc		333
Asp	Gly	Gly	Phe	Leu	Thr	Ala	His	Gln	Asp	Thr	Ser	Leu	Asp	Gly		
			100					105					110			

<210> 1057

<211> 111

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; KFP F1D, with position 1 Met removed

<400> 1057

Ala	Ser	Leu	Leu	Thr	Glu	Thr	Met	Pro	Phe	Lys	Thr	Thr	Ile	Glu	Gly
1				5					10					15	

Thr	Val	Asn	Gly	His	Cys	Phe	Lys	Cys	Ile	Gly	Lys	Gly	Glu	Gly	Asn
			20					25					30		

Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly

35

40

45

Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly
50 55 60

Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys
65 70 75 80

Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu
85 90 95

Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly
100 105 110

<210> 1058

<211> 363

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; KFP F2D, with Met added @ position 1

<220>

<221> CDS

<222> (1)..(363)

<223> KFP F2D corresponds to aa residues 113-end of KFP1

<400> 1058

atg gac tgc ctg gtg tac aag gtg aag atc ctg ggt aac aac ttc ccc 48
Met Asp Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro
1 5 10 15

gcc gac ggc ccc gtg atg cag aac aag gtc ggc cgc tgg gag ccc gga 96
Ala Asp Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly
20 25 30

acc gag atc gtg tac gag gtg gac ggc gtg ctg cgc ggc cag tcc ctg 144
Thr Glu Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu
35 40 45

atg gcc ctg aag tgc ccc ggc ggc cgg cac ctg acc tgc cac ctg cac 192
Met Ala Leu Lys Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His
50 55 60

acc acc tac cgc tcc aag aag ccc gcc tcc gcc ctg aag atg ccc ggc 240
Thr Thr Tyr Arg Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly
65 70 75 80

ttc cac ttc gag gac cac cgc atc gag atc atg gag gag gtg gag aag 288
Phe His Phe Glu Asp His Arg Ile Glu Ile Met Glu Glu Val Glu Lys
85 90 95

ggc aag tgc tac aag cag tac gag gcc gcc gtg ggc cgc tac tgc gac 336
Gly Lys Cys Tyr Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp
100 105 110

gcc gcc ccc tcc aag ctg ggc cac aac
 Ala Ala Pro Ser Lys Leu Gly His Asn
 115 120

<210> 1059
 <211> 121
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; KFP F2D, with Met added @ position 1

<400> 1059

Met Asp Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro
 1 5 10 15

Ala Asp Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly
 20 25 30

Thr Glu Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu
 35 40 45

Met Ala Leu Lys Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His
 50 55 60

Thr Thr Tyr Arg Ser Lys Lys Pro Ala Ser Ala Leu Lys Met Pro Gly
 65 70 75 80

Phe His Phe Glu Asp His Arg Ile Glu Ile Met Glu Glu Val Glu Lys
 85 90 95

Gly Lys Cys Tyr Lys Gln Tyr Glu Ala Ala Val Gly Arg Tyr Cys Asp
 100 105 110

Ala Ala Pro Ser Lys Leu Gly His Asn
 115 120

<210> 1060
 <211> 504
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; KFP F1E, with position 1 Met removed

<220>
 <221> CDS
 <222> (1)..(504)
 <223> KFP F1E corresponds to aa residues 1-169 of KFP1

<400> 1060
gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag ggc 48
Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly
1 5 10 15
acc gtg aac ggc cac tgc ttc aag tgc atc ggc aag ggc gag ggc aac 96
Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn
20 25 30
ccc ttc gag ggc acc cag gag atg aag atc gag gtg atc gag ggc ggc 144
Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly
35 40 45
ccc ctg ccc ttc gcc ttc cac atc ctg tcc acc tcc tgc atg tac ggc 192
Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly
50 55 60
tcc aag acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc aag 240
Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys
65 70 75 80
cag tcc ttc ccc gag ggc ttc acc tgg gag cgc acc acc acc tac gag 288
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu
85 90 95
gac ggc ggc ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc gac 336
Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp
100 105 110
tgc ctg gtg tac aag gtg aag atc ctg ggt aac aac ttc ccc gcc gac 384
Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp
115 120 125
ggc ccc gtg atg cag aac aag gtc ggc cgc tgg gag ccc gga acc gag 432
Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu
130 135 140
atc gtg tac gag gtg gac ggc gtg ctg cgc ggc cag tcc ctg atg gcc 480
Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala
145 150 155 160
ctg aag tgc ccc ggc ggc cgg cac 504
Leu Lys Cys Pro Gly Gly Arg His
165

<210> 1061
<211> 168
<212> PRT
<213> Artificial

<220>
<223> modif. frag.; KFP F1E, with position 1 Met removed

<400> 1061

Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly
1 5 10 15

Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn
 20 25 30

Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly
 35 40 45

Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly
 50 55 60

Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys
 65 70 75 80

Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu
 85 90 95

Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp
 100 105 110

Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp
 115 120 125

Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu
 130 135 140

Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala
 145 150 155 160

Leu Lys Cys Pro Gly Gly Arg His
 165

<210> 1062

<211> 192

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; KFP F2E, with Met added @ position 1

<220>

<221> CDS

<222> (1)..(192)

<223> KFP F2E corresponds to aa residues 170-end of KFP1

<400> 1062

atg ctg acc tgc cac ctg cac acc acc tac cgc tcc aag aag ccc gcc
 Met Leu Thr Cys His Leu His Thr Thr Tyr Arg Ser Lys Lys Pro Ala
 1 5 10 15

48

tcc gcc ctg aag atg ccc ggc ttc cac ttc gag gac cac cgc atc gag	96
Ser Ala Leu Lys Met Pro Gly Phe His Phe Glu Asp His Arg Ile Glu	
20 25 30	

atc atg gag gag gtg gag aag ggc aag tgc tac aag cag tac gag gcc	144
Ile Met Glu Glu Val Glu Lys Gly Lys Cys Tyr Lys Gln Tyr Glu Ala	
35 40 45	

gcc gtg ggc cgc tac tgc gac gcc gcc ccc tcc aag ctg ggc cac aac	192
Ala Val Gly Arg Tyr Cys Asp Ala Ala Pro Ser Lys Leu Gly His Asn	
50 55 60	

<210> 1063
 <211> 64
 <212> PRT
 <213> Artificial

<220>
 <223> modif. frag.; KFP F2E, with Met added @ position 1

<400> 1063

Met Leu Thr Cys His Leu His Thr Thr Tyr Arg Ser Lys Lys Pro Ala
1 5 10 15

Ser Ala Leu Lys Met Pro Gly Phe His Phe Glu Asp His Arg Ile Glu
20 25 30

Ile Met Glu Glu Val Glu Lys Gly Lys Cys Tyr Lys Gln Tyr Glu Ala
35 40 45

Ala Val Gly Arg Tyr Cys Asp Ala Ala Pro Ser Lys Leu Gly His Asn
50 55 60

<210> 1064
 <211> 555
 <212> DNA
 <213> Artificial

<220>
 <223> modif. frag.; KFP F1F, with position 1 Met removed

<220>
 <221> CDS
 <222> (1)..(555)
 <223> KFP F1F corresponds to aa residues 1-186 of KFP1

<400> 1064	
gcc tcc ctg ctg acc gag acc atg ccc ttc aag acc acc atc gag gcc	48
Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly	
1 5 10 15	

acc gtg aac ggc cac tgc ttc aag tgc atc ggc aag ggc gag ggc aac	96
Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn	
20 25 30	
ccc ttc gag ggc acc cag gag atg aag atc gag gtg atc gag ggc ggc	144
Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly	
35 40 45	
ccc ctg ccc ttc gcc ttc cac atc ctg tcc acc tcc tgc atg tac ggc	192
Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly	
50 55 60	
tcc aag acc ttc atc aag tac gtg tcc ggc atc ccc gac tac ttc aag	240
Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys	
65 70 75 80	
cag tcc ttc ccc gag ggc ttc acc tgg gag cgc acc acc acc tac gag	288
Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu	
85 90 95	
gac ggc ggc ttc ctg acc gcc cac cag gac acc tcc ctg gac ggc gac	336
Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp	
100 105 110	
tgc ctg gtg tac aag gtg aag atc ctg ggt aac aac ttc ccc gcc gac	384
Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp	
115 120 125	
ggc ccc gtg atg cag aac aag gtc ggc cgc tgg gag ccc gga acc gag	432
Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu	
130 135 140	
atc gtg tac gag gtg gac ggc gtg ctg cgc ggc cag tcc ctg atg gcc	480
Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala	
145 150 155 160	
ctg aag tgc ccc ggc ggc cgg cac ctg acc tgc cac ctg cac acc acc	528
Leu Lys Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr Thr	
165 170 175	
tac cgc tcc aag aag ccc gcc tcc gcc	555
Tyr Arg Ser Lys Lys Pro Ala Ser Ala	
180 185	

<210> 1065

<211> 185

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; KFP F1F, with position 1 Met removed

<400> 1065

Ala Ser Leu Leu Thr Glu Thr Met Pro Phe Lys Thr Thr Ile Glu Gly
1 5 10 15

Thr Val Asn Gly His Cys Phe Lys Cys Ile Gly Lys Gly Glu Gly Asn
 20 25 30

Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly Gly
 35 40 45

Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr Gly
 50 55 60

Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe Lys
 65 70 75 80

Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr Glu
 85 90 95

Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly Asp
 100 105 110

Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala Asp
 115 120 125

Gly Pro Val Met Gln Asn Lys Val Gly Arg Trp Glu Pro Gly Thr Glu
 130 135 140

Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met Ala
 145 150 155 160

Leu Lys Cys Pro Gly Gly Arg His Leu Thr Cys His Leu His Thr Thr
 165 170 175

Tyr Arg Ser Lys Lys Pro Ala Ser Ala
 180 185

<210> 1066

<211> 141

<212> DNA

<213> Artificial

<220>

<223> modif. frag.; KFP F2F, with Met added @ position 1

<220>

<221> CDS

<222> (1)..(141)

<223> KFP F2F corresponds to aa residues 187-end of KFP1

<400> 1066
 atg ctg aag atg ccc ggc ttc cac ttc gag gac cac cgc atc gag atc 48
 Met Leu Lys Met Pro Gly Phe His Phe Glu Asp His Arg Ile Glu Ile
 1 5 10 15

atg gag gag gtg gag aag ggc aag tgc tac aag cag tac gag gcc gcc 96
 Met Glu Glu Val Glu Lys Gly Lys Cys Tyr Lys Gln Tyr Glu Ala Ala
 20 25 30

gtg ggc cgc tac tgc gac gcc gcc ccc tcc aag ctg ggc cac aac 141
 Val Gly Arg Tyr Cys Asp Ala Ala Pro Ser Lys Leu Gly His Asn
 35 40 45

<210> 1067

<211> 47

<212> PRT

<213> Artificial

<220>

<223> modif. frag.; KFP F2F, with Met added @ position 1

<400> 1067

Met Leu Lys Met Pro Gly Phe His Phe Glu Asp His Arg Ile Glu Ile
 1 5 10 15

Met Glu Glu Val Glu Lys Gly Lys Cys Tyr Lys Gln Tyr Glu Ala Ala
 20 25 30

Val Gly Arg Tyr Cys Asp Ala Ala Pro Ser Lys Leu Gly His Asn
 35 40 45